InterPro; IPR000504; RNA_rec_mot.

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RESULT 15
Q7XUKB
ID Q7XUKB
AC Q7XUK
AC Q7XUK
DT 01-OC
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GN OSJNB
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Q8MYR3
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Best Local S
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Best Local Similarity
Matches 8; Conserv
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InterPro; IPR006630; Lupus_La_dom.
Pfam; PF05383; La; 1.
SMART; SM00715; LA; 1.
NON TER 269 269
SEQUENCE 269 AA; 29223 MW; 52951
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01-OCT-2002
01-OCT-2002
01-OCT-2003
                                                                                                                                        OTXUK8;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
05)NBa0067K08.21 protein.
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                          Oryza sativa (Rice).

Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 206 AA; 23992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF05383; La; 1
Pfam; PF00076; rrm;
                                                                                                                           OSJNBA0067K08.21.
                                                                                                                                                                                                                                                                                 Q7XUK8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERAIIRQVEYYF-----GDF 16
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
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57.1%;
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Last sequence update)
Last annotation update)
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Pred. No. 8.1;
2; Mismatches
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Last annotation update)
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Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.
Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.
Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
Huang Y.C., Li Y., Zhu J.J., Zhang L., Liu Y.L., Mu J. Yu Z.,
Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
Zhang R.Q., Guan J.P., Hong G.F.;
Shubitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AL606627, CAM1244.1; -
17 KEVLROVEFYFSD
                                    3 RAIIRQVEYYEGD 15
                                                                        7;
                                                                                           Similarity
                                                                                                                                               435 AA;
                                                                        Conservative
                                                                                                                                               41244.1; -.
48295 MW; 66BA0B471B0AE119 CRC64;
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53.8%;
 29
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Pred. No.
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13;
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Best Local S
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Matches
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InterPro; IPR00630; Lupus_La.
InterPro; IPR00630; Lupus_La.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF005076; rrm; 1.
PRINTS; PR00305; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                   065529
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EMBL, BY00396, AAM96968.1; --
EMBL, BY00396, AAM9698.1; --
EMBL, BY00396, AAM15715.1; --
EMBL, BY00396, AAM9698.1; --
EMBL, BY00396, AAM9698, A
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Submitted
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2002
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                                                                                                                                                                                                                              KTVLRQVEFYFSD
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                                                                       PRELIMINARY;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                          Score 48; DB
Pred. No. 8.9;
4; Mismatches
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Pred. No. 8.9;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                             4.
                                                                       PRT;
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9.9;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
L'Ecuyer T.J., Fang H.-L.;
L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMBL/GenBar
Submitted NAL70269.1; -.
R EMBL; AF467897; AAL70269.1; -.
R GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
ThterPro; IPR002344; Lupus La.
ThterPro; IPR0023630; Lupus La.
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Best Local S
Matches 7
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Mewes H.W., Mayer K.F.
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Hypothetical |
SEQUENCE 48
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BEVAIN M., Benes V., Rechmann S., I

Hevan M., Mayer K.F.X., Schuell

Mewes H.W., Mayer K.F.X. the EMBL/
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01-AUG-1998
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submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL022537; CAA18589.1; -
EMBL; AL161582; CAB79989.1; -
PIR; T04453; T04453.
                                                                                                                                                                                                                                                                                                                                                                       UBP.

Gallus gallus (Chicken).

Gallus gallus (Chicken).

Craniata; Vert

Corrota; Metazoa; Chordata; Craniata; Vert

Corrota; Metazoa; Chordata; Galliformes;
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#4D11.80 OR AT4G32720.

rabidopsis thaliana (Mouse-ear cress).

Rukaryota; Viridiplantae; Streptophyta; Embryophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core ev

eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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Mayer K.F.X.;
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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InterPro; IPR002344; Lupus_La.
InterPro; IPR006530; Lupus La.
InterPro; IPR000504; RNA_rec_mot.
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483 AA; 5
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Pred. No. 9.9;
4; Mismatches
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ler C.;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR00630; Lupus La_dom.
InterPro; IPR006530; Lupus La_dom.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF05383; La; 1.
Pfam; PF00376; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00715; LA; 42100 MW;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poalea;
Ehrhartoideae; Oryzeae; Oryza.
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.

PROSITE; PS00030; RRM_RMP_1; A2D828A4AFAA3C34 CRC64;

SEQUENCE 396 AA; 43631 MW; A2D828A4AFAA3C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2001) to the EMBL; AP003375; BAB90138.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF003140; AAB54169.1; -. PIR; T30953; T30953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gramene; Q8S0T8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002344; Lupus_La_dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone:OJ1414_E05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005634; C:nucleus; IEA. GO:0003723; F:RNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF05383; La;
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8; Conserv
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8; Conserv
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                                                                                                                                                                             IVKQVEYYFSD 101
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(TrEMBLrel.
                                                                                                                                                                                                                                                                               Conservative
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                                                  PRELIMINARY;
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24,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                          Score 49; DB 1
Pred. No. 5.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases.
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                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                10C1863EAB6FA7B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEA.
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RESULT 10
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Best Local S
Matches 8
                Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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Q93ZV7;
Q1-DEC-2001
Q1-DEC-2001
Q1-OCT-2003
                                                                                                                                                                                                                                "Full Length cDNA of gene AT4g32720 (GI:7270219).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY056237; AAL07086.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005723; F:RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Yamada K., Banh J., Banno F., Dale J.M., Yamamura Y., Yu G., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Kawai J., Kim C., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
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Submitted (FEB-2003) to the EMB
EMBL; BC046654; AAH46654.1; -
GO; GC:0005534; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last ann
Similar to lupus LA protein homolog
Xenopus laevis (African clawed frog)
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InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                         InterPro;
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                                                                                                                                                          [nterPro;
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                                                                                                                                                    IPR002344; Lupus_La.
IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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72.7%;
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Last annotation updat
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Pred. No.
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Matches
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Varidiplantae; eudicotyledons; core e
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Tabata S.
  SEQUENCE FROM N.A. Shinn P., Chen H., Cheuk R., Kim Banh J., Bowser L., Carninci P., Hayashizaki Y., Ishida J., Jiang Karlin-Neumann G., Kawai J., Lam
                                                                                                                   Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidu eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI TaxID=3702;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana features of the regions of 1,381,565 bp cover physically assigned P1 and TAC clones."; DNA Res. 5:131-145(1998)
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SM00715; LA; 1.
SM00360; RRM; 1.
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Ig P.X., Jones T., Kamiya
.m B., Lee J.M., Lin J.,
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Pham P.K., Quach H.L., Sakurai T., Satou M., Sa
Tang C.C., Toriumi M., Yamada K., Yamamura Y.,
Shinozaki K., Davis R.W., Theologis A., Ecker ("Arabidopsis cDNA clones.";
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SEQUENCE FROM N.A. STRAIN=Bristol N2; Waterston R.;
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GO; GO:0003723; F:RNA binding; IEA
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InterPro; IPR006630; Lupus La_dom.
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X MEDLINE-21085660; pubMed=1121781;

XA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Alzawa K., Matsuda Y., Nikaido I., Pesole G., Quackenbush J.,

XA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

XA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

XA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

XA Schriml L.M., Staubli F., Suzuki R., Tomita M., Washio T.,

XA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

XA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

XA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

XA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

XA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

XA Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Scorch K.-F.,

XA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havashizaki Y., Stortsuki S.,

Havashizaki Y., Stortsuki S.,
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Best Local S
Matches 15
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Best Local
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09CYB9;
01-JUN-2001
01-JUN-2001
01-OCT-2003
Q8BTU4;
Q8BTU4;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK017822; BAB30957.1; -.
MGD; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus_La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO03
SMART; SM0071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF05383; La; 1.
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15; Conservative
                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                    ERAIIRQVEYYFGDF 16
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IPR000504;
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1 (TrEMBLrel. 17,
3 (TrEMBLrel. 25,
ndrome antigen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                    381 AA;
(TrEMBLrel.
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Lupus_La.
; Lupus_La_dom.
; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                    43891 MW;
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23,
23,
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Pred. No. 5.9e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   Score 57; L
Pred. No. 0.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2E2DEF1452C0F0E9 CRC64;
                                                                                                                                                                                                                                                                                                                         Mismatches
sequence update)
                                                                                 415
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RESULT 4
Q7ZTIO
ID Q7ZT
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Best Local S
Matches 10
Query Match
                                                                                                                                                                                              Submitted (JAN-2003) to the EMBL/GenE
EMBL; BC045392; AAH45392.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR006304; Lupus_La.
InterPro; IPR006301; Lupus_La dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7ZTIO;
01-JUN-2003 (
01-JUN-2003 (
01-OCT-2003 (
                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; El
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to sjogren syndrome antigen B (Autoantigen
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 415 AA; 47657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
BMBL, AK088677; BAC40498.1; -.
MGD, MGI.98423, SSb.
GO; GO:0005634; C:nucleus; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25,
                                                                                                             Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7ZTI0
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Pfam; PF00076; rrm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sjogren syndrome antigen ssm.
                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mûs musculus
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Body;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7955;
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IPR006630; Lupus La dom.
IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
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  63.18;
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                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
  Score 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                             2EF032FDD3916291 CRC64;
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Length 401;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                             SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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84
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137.751 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
sp_organelle:*
sp_phage:*
sp_phant:*
sp_vente:*
sp_ventes:*
sp_vertebrate:*
sp_vertebrate:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                         sp_human:*
sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Query Match Length	DB	ID	Description
_	78	92.9	390	S	Q8T8V5	Q8t8v5 drosophila
N	57	67.9	381	11	09СҮВЭ	Q9cyb9 mus musculu
ω	57	67.9	415	드	Q8BTU4	Q8btu4 mus musculu
4	53	63.1	401	13	Q7ZTI0	Q7zti0 brachydanio
יט	53	63.1	411	10	Q9FL36	Q9fl36 arabidopsis
6	53	63.1	422	10	Q94A38	Q94a38 arabidopsis
7	50	59.5	396	5	001806	001806 caenorhabdi
8	49	58.3	389	10	Q8SOT8	Q8s0t8 oryza sativ
ø	48	57.1	427	13	Q7ZTK2	Q7ztk2 xenopus
10	48	57.1	433	10	Q93ZV7	Q93zv7 arabidopsi
11	48	57.1	433	10	Q8L7E4	Q817e4 arabidopsi
12	48	57.1	483	10	065529	O65529 arabidopsis
13	47	56.0	206	13	Q8QHI5	Q8qhi5 gallus gal
14	47	56.0	269	ហ	Q8MYR3	Q8myr3 drosophila
15	47	56.0	435	10	Q7XUK8	Q7xuk8 oryza sativ
16	47	76.0	n n	,		

ALIGNMENTS

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YJGN ECOLI STANDARU;
ID YJGN ECOLI STANDARU;
AC 93938; P39339; P76811;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yjgN.

"""N OR B4257.

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""" Gammaproteobacteria;
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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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Nature 409:529-533(2001).
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                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia
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Welch R.A., Blattner F.R.;
REVISIONS
                                         "Analysis of the Escherichia coli genome VI: DNA sequence region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                             SEQUENCE FROM N.A
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Tanaka M., Tobe T.,
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                              EMBL; U14003; AAA97153.1; ALT_FRAME.
EMBL; U14003; AAA97154.1; ALT_FRAME.
EMBL; AE000496; AAC77214.1; ALT_FRAM
                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rudd K.E.;
Unpublished observations (JAN-2000).
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997):
                                                                                                                                                                                                                                                    EcoGene;
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RA Bargues M., Baron L., Becker A., Biteau N., Bahr A., Ballesta J.P.G., RA Bargues M., Baron L., Becker A., Biteau N., Bloecker H., Blugeon C., Ra Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F., Ra Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F., Ra Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F., Ra Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F., Ra Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T., Ra Hoheisel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C., Ra Hoheisel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C., Ra Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Ricker S., Ra Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N., Ra Paulin L., Perea J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M., Ra Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L., Paricio M., Schaefer M., Schmidt E.R., Schneider C., Scholler P., Schwarz S., Schwarz S., Voet M., Schwarz S., Schwarz S., Voet M., Schwarz S., Schwarz S., Voet M., Volckaert G., Ra Wagner G., Wambutt R., Wedler E., Wedler H., Woelfi S., Harris D.E., Ra Wagner G., Wambutt R., Wedler E., Wedler H., Woelfi S., Harris D.E., Ra Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S., Ra Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S., Ra Manlin N., Huni S., Johnston F.S., Mulligan J.T., Allen E., Ra Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Ra Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Ra Araujo R., Shroff N., Winant A., Yelton M.A., Botstein D., Berthan S., Schroeder M., Ra Araujo R., Fulton M., Andrews S., Brinkman R., Copper J., Ding H., Ra Hollish K., Fulton M., Andrews S., Brinkman R., Copper J., Ding H., Ra Hollish K., Fulton M., Andrews S., Brinkman R., Copper J., Ding H., Ra Hollish K., Wambat T., Langston Y., Latreille P., Le T., Mardis E., Ra Menezes S., Miller L., Tarich A., Teraskis E., Vignati D., Wilcox L., Wohldman P., Tarich A., Teraski
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La.";
MEDLINE=94012814; PubMede8408076;
Nagiec M.M., Wells G.B., Lester R.L., Dickson R.C.;
"A suppressor gene that enables Saccharomyces cerevisiae to grow without making sphingolipids encodes a protein that resembles an Escherichia coli fatty acyltransferase.";
J. Biol. Chem. 268:22156-22163(1993).
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01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
La protein homolog (La ribonucleoprotein) (
LAH1 OR LHP1 OR YLA1 OR YDL051W.
                                                                                                                                                                                                         MEDLINE=95097387;
Lin-Marq N., Clarl
"A yeast RNA bind:
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Kleine K., Mewes H.-W., Zoll
"The nucleotide sequence of
Nature 387:75-78(1997).
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RESULT 14
YJGN_ECOS
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Matches
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Unpublished c
                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Create
16-OCT-2001 (Rel. 40, Last &
28-FEB-2003 (Rel. 41, Last &
Hypothetical protein yjgN.
YJGN OR Z5869 OR ECS5234.
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L33023; AAA21777.1; EMBL; Z74099; CAA98612.1; - EMBL; L13282; AAA16515.1; EMBL; X80801; CAA56782.1; - PIR; B48600; B48600.
                                                                                                                                                                                                                                                                                                                                                                  ECOS7
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Germonline; 140293; -.
SGD; S0002209; LHP1.
GO; GO:0005730; C:nucleolus; IDA.
GO; GO:0005654; C:nucleoplasm; IDA.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0003723; F:RNA binding; IMP.
STRAIN=0157:H7 / EDL933 / ATCC 700927; MEDLLNE=21074935; PubMed=11206551; Perna N.T., Plunkett G. III, Burland V., Rose D.J., Mayhew G.F., Evans P.S., Gregg Posfai G., Hackett J., Klink S., Boutin J
                                                                                                                                                                                                                                                                                                                        P58219;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEGRNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                         SEQUENCE
                                                                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 RNA recognitio SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Binds to the precursors of polymerase preferentially to precursors ending in U residue SUBCELLULAR LOCATION: Nuclear (Probable)
                                                                                                                                                   _TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                    ECO57
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6; Conserv
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240
275 AA;
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Bioinformatics Institute. The
-profit institutions as long
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32104
                                                                                                                                                                       teria; Gammaproteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.5%;
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                                                                                                                                                                                                                                                                                 annotation
                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB:
Pred. No. 5.8;
4; Mismatches
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****CTLEAR LOCALIZATION SIGNAL
*****CTLEAR LOCALIZATION CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Bioinformatics
  Burland V., Mau B., Glasner J.D
P.S., Gregor J., Kirkpatrick H
S., Boutin A., Shao Y., Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    It is produced
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                                                                                                                                                                                                                                                                                 update)
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MBL outstation -
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C STRAINEV. COLUMDIA;

X MEDLINE=21016719; PubMed=11130712;

X MEDLINE=21016719; PubMed=1130712;

X MEDLINE=21016719; PubMed=11130712;

X MEDLINE=21016719; PubMed=1130712;

X MEDLINE=21016719; PubMed=113071
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VP45_ARATE
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Best Local S
Matches 7
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Vacuolar protein-sorting protein 45 homolog (
VPS45 OR ATIG77140 OR T14N5_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotytaedons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;
MEDLINE=98289086; PubMed=9625693;
Bassham D.C., Raikhel N.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GermOnline; 138873; -. SGD; S0000542; SRO9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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GO:0003723; F:RNA binding; IDA.
GO:0006412; P:protein biosynthesis;
erPro; IRR006630; Lupus_La_dom.
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466 AA;
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  Van Aken S.,
Fraser C.M.,
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51789
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63.6%;
Tambunga G., Toriumi M.J., Town C.D en S., Vaysberg M., Vysotskaia V.S., C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
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Pred. No. 6.
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POLY-ASN.
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6.7;
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                                                                                                                                                                                                                                                                                                       Dewar K.,
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Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

Bouthwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Karlin Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Karlin Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Karlin Newmann G., Liu S.X., Lam B., Chang C.H., Lee J.M., Toriumi M.J.,

Khan M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Anno F., Boddsmith A.D., Gurijal M., Hansen N.F.,

A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                          Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Involved in the protein transport to the vacuole, probably at the level of vesicle fusion at the trans-Golgi network (TGN) and not in transport from the TGN to the prevacuolar compartment. Binds syntaxins.

C:- SUBUNIT: Interacts with both SYP41 or SYP42 and VTI12, but in different domains of the trans-Golgi network. Does not interact the pervacuolar compartment with VTI11, SYP21 or SYP22, or on the gervacuolar compartment with VTI11, SYP21 or SYP22, or on the Golgi with SYP31.

C:- SUBCELLULAR LOCATION: Peripheral membrane protein. Binds to trans-Golgi network membranes through interaction with other proteins Golgi network membranes through interaction with other proteins c:- SIMILARITY: Belongs to the STXBP/UNC-18/SEC1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF036234; AAC39472.1; -.
EMBL; AC004260; AAC34344.1; -.
EMBL; AY005070; AAK91388.1; -.
EMBL; AY101517; AAM26638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstations the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annousentities requires agreement (See http://www.isb-sib.ch/annousentities agreement (See http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bassham D.C., Sanderfoot A.A., Kovaleva V., Zl "AtVPS45 complex formation at the trans-Golgi Mol. Biol. Cell 11:2251-2265(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                   Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001619; Sec1-like
Pfam; PF00995; Sec1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20346955; PubMed=10888666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22954850; PubMed=14593172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T00445; T00445.
T52056; T52056.
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408:816-820(2000).
                                                                        N
                                                                                                                                                          Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302:842-846(2003).
                                                                             ERAIIRQVEYYFGDF
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                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                        transport; Golgi stack; Multigene family.
362 T -> I (IN REF. 1).
64942 MW; 844F24C9A21E9C1D CRC64;
                                                                                                                                                                                                     51.2%;
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                                                                                                                                                              6
                                                                                                                                                                                                     Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kovaleva V.,
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                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zheng
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                                                                                                                                                                                                                                               Length 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ.
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L outstation -
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InterPro; IPR002344; InterPro; IPR006630;

InterPro; IPR000504;

GeneDB

SPombe;

SPAC57A10.10c; -.

PIR; T43542; T43542

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RESULT 10
HO2_RAT
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Best Local
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P23711;
01-NOV-1991 (Rel. 2
01-NOV-1991 (Rel. 2
15-MAR-2004 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
SMART; S
                                                                                                   "Evidence suggesting that the two forms of heme oxygenase are products of different genes";
J. Biol. Chem. 263:3348-3353(1988).
-i- FUNCTION: Heme oxygenase cleaves the heme ring at the alp methene bridge to form biliverdin. Biliverdin is subseque converted to bilirubin by biliverdin reductase. Under physiological conditions, the activity of heme oxygenase highest in the spleen, where senescent erythrocytes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rotenberg M.O., Maines M.D.;
"Isolation, characterization, and expression in Escherichia coli of cDNA encoding rat heme oxygenase-2.";
J. Biol. Chem. 265:7501-7506(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG
                                                                  <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                 encoding rat heme oxyo
Gene 139:155-161(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Liver; MEDLINE=94156193; PubMed=8112599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-binding; Nuclear protein
                                                                                                                                                                                                                                                                                                  Cruse I., Maines M.D.;
                                                                                                                                                                                                                                                                                                                        MEDLINE=88139412; PubMed=3343248;
                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver,
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 142-232 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The structure, organization and differential expression of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCoubrey W.K. Jr., Maines M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90237051; PubMed=2185251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                               sequestrated and destroyed. FUNCTION: Heme oxygenase 2
                          neurotransmitter.
                                            of carbon monoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PR00302; LUPUSLA.
SM00715; LA; 1.
SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                               and Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          el. 20, Created)
el. 20, Last sequence update)
el. 43, Last annotation update)
2 (EC 1.14.99.3) (HO-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         oxygenase-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Lupus La.
; Lupus La_dom.
; RNA_rec_mot.
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                                            brain where
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Pred. No. 1.2;
4; Mismatches
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  + 3 AH(2)
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                                          could be in where it
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                                                                                                                                                                                                                                                                                                                                                                    PARTIAL
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  + 0(2)
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could act
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iniverdin is subsequently
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  biliverdin + Fe(2+)
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                   SRO9_YEAST
225567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J05405; AAA41340.1;
EMBL; U05013; AAA19130.1;
EMBL; M18918; AAA41347.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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                                         interactions with tropomyosin genes, su
organization of the actin cytoskeleton.
Genetics 147:1003-1016(1997).
-I- FUNCTION: May overlap in function w
                                                                                     Kagami M., Toh-E A., Matsui Y.; "SRO9, a multicopy suppressor of the bud growth defect in the Saccharomyces cerevisiae RHO3-deficient cells, shows strong go
                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                             01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01126; Heme_oxygenase; 1.
PRINTS; PR00088; HAEMOXYGNASE.
PROSITE; PS00593; HEME_OXYGENASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A35199; A35199.
HSSP; P06762; 1DVG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                       MEDLINE=98043396;
                                                                                                                                   CHARACTERIZATION.
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                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00595; name Grace, Multigene fam
Heme; Oxidoreductase; Microsome; Multigene fam
IRON (HEME AXIAL
                                                                                                                                                                                                                                                                    10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
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SUBCELLULAR LOCATION: Micro
TISSUE SPECIFICITY: Widely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the heme oxygenase family.
SIMILARITY: Contains 2 heme regulatory motif (HRM) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
         suppressor of SIMILARITY: So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           concentration in the brain.
INDUCTION: Heme oxygenase 2 activity is non-inducible.
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                                 involved in organization of
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1., Esteban
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                                                                                                                                                                                                                                                                     annotation
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Pred. No.
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HRM 2.
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                                  filaments.
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Matches 8
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01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-MAR-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol. Biol. 231:196-204(1993).

-I- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription terminatic factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).

-I- SUBCELLULAR LOCATION: Nuclear (Probable).
-I- DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly constant steady state level in mature occytes, eggs, and early
                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                       PROSITE; PS50102; RRM, 1. 1.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Nuclear protein; P
RNA-binding; Nuclear protein; P
DOMAIN 111 203 RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93287095; PubMed=8510143; Scherly D., Stutz F., Lin-Marq N. "La proteins from Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAA XENLA
                                                                                                                                                                                                                  SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                             PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                                                                                            Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                         InterPro; IPR006630;
InterPro; IPR000504;
                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                EMBL; X68817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
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NCBI_TaxID=8355;
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                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN. SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embryos.
17
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                                                    Similarity
8; Conserv
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ICEQIEYYFGD
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                                                      Conservative
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    Last sequence update)
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    Last annotation update

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GH, TO MAMMALIAN LA PROTEIN.
27
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                                                                                                                                                                                                                                                                                      Lupus_La_dom.
RNA_rec_mot.
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opus laevis. cDNA cloning
                                                                                                                 ¥.
                                                                                                           ; Phosphorylation.
RNA-BINDING (RRM).
NUCLEAR LOCALIZATION SIGNAL
NUCLEAR LOCALIZATION SIGNAL
, AEB3A38B7DZE3EC3 CRC64;
                                                                     Score 48; I
Pred. No. 0
                                                       Mismatches
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                                                                                   DB 1;
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RA Sgours J., Peat N., Mayles J., Bakham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Ritherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Fundom M., Squares R., Squares S., Stevens K.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Berr P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galbert M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAH1 SCHPO STANDARD; PRT; 298 AA. P87058; O13362; Q10458; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) La protein homology (La ribonucleoprotein) (La SLA1 OR SPAC57A10.10C.
                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
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                                 EMBL; AF022949; AAB82145.1; -. EMBL; AB011371; BAA24981.1; -.
                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                              dispensable phosphoprotein that functions in tRNA maturation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98067398; PubMed=9404894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wood V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1998)
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                                                                                                                                                                                                                                                                                                     -1- FUNCTION: Binds to the precursors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van Horn D.J., Yoo C.J., Xue D., Shi H., Wolin 9
"The La protein in Schizosaccharomyces pombe: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                AB011371;
Z94864; CF
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R., Rajandream M.A.,
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Baker S., Basham
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SEQUENCE

415 AA;

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1; 1.
ein; Phosphorylation.
exnA-BINDING (RRM).
MW; 033FD9CC1E475F98 CRC64;

DB 1;

Length 415;

SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS001030; RRM; RNP 1; 1.
RNA-binding; Nuclear protein; Pt RNA-binding; Nuclear Protein; RNA-binding; Nuclear Protein; Pt RNA-binding; Nuclear Protein; Nuclear Protein; Nuclear Protei

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EASTIRQLEYYFGD

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RESULT 6
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Best Local &
                                              Query Match
Best Local
                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                               Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q26457;
15-JUL-1998
                                                                                                                                             PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=96135233; PubMed=8551578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
                                                                                             PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; FALSE NEG.
RNA-binding; Nuclear protein; DNA-Bindi
DOMAIN 141 228 RNA-BINDII
                                                                                                                                                                                                     InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                           EMBL; S80954; AAB35931.1; -
                                                                                                                                                                                                                                                                 entities requires a license agreement or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                        use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LA_AEDAL
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Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                         Thie
                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                              amounts are present in the cytoplasm. SIMILARITY: Contains 1 RNA recognition motif (RRM) SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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           ERAIIRQVEYYFGD
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66.7%;
                                               66.7%;
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                                                                                  ₩,
                                    Score 56; DB Pred. No. 0.02 2; Mismatches
                                                                                  ; DNA-Binding.
RNA-BINDING (RRM).
; 4E5CC8F21C40F452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 1;
Pred. No. 0.021;
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                                                             DB 1;
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                                               .028;
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                                                          Length 383;
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Matches 8
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                                                                                                      SMART; SM0036U; AMERICAL SMART; SM0036U; AMERICAL SMART; SM0036U; AMERICAL SMART; I. FALSE NEG.
PROSITE; PS00030; ARM RNP 1; FALSE NEG.
PRO-BITTS PS00030; ARM RNP 1; FALSE NEG.
RNA-BINDING (RRM).
DOMAIN 110 202 RNA-BINDING (RRM).
DOMAIN 315 331 MUCLEAR LOCALIZATION
A995 MW; 45F3146F8934A355 CF
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992
01-AUG-1992
15-MAR-2004
Lupus La prot
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P28049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression.";

J. MOL. Biol. 231:196-204(1993).

I. FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts (By similarity).
polymerase III transcripts (By similarity).
1- SUBCELLULAR LOCATION: Nuclear (Probable).
1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes,
accumulate in stage III/IV occytes, then exhibit a roughly
                                                                                                                                                                                                                                                         InterPro; IPR002344; Lupus_La.
InterPro; IPR00630; Lupus_La_dom.
InterPro; IPR000630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                         EMBL; X68818; CAA48716.1; -. PIR; S33817; S33817.
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"La proteins from Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93287095; PubMed=8510143;
Scherly D., Stutz F., Lin-Marq N.,
"La proteins from Xenopus laevis. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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16
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                                                           Similarity
8; Conser
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                              IIRQVEYYFGD
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                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 23, Created)
. 23, Last sequence update)
. 43, Last annotation update)
. homolog B (La ribonucleoprotein B) (La autoantigen
                                                                           57.1%;
72.7%;
                              15
 26
                                                            Score 48; DB
Pred. No. 0.81
1; Mismatches
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                                                              Gaps
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RC STRAIN-FVB/N. TISSUE-Mammary gland;

RX MEDLINE-22388257; pubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Strausberg R.L., Feingold E.A., Grouse L.H., Schuler G.D.,

RX Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheet T.E.,

RX Altschal S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Alchards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alchards S., K., K., K., K.J., Malchards S., Sanchez A.,

RX Alchards S., K., K., K., K., Marra M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Groelz D., Bachmann M.;

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including the polymerase including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts including the procursor form of RNA polymerase III transcripts in the procursor form of RNA polymerase III transcripts in the polymerase III transcripts in the polymerase III transcripts in the polymeras
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                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrement of Bioinformatics and the Entrement Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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SEQUENCE FROM N.A.
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01-OCT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
                                                                                           EMBL; L00993; AAA39415.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR SS-B.
                            BC003820; AAH03820.:
Y07951; CAA69249.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .7-2 RNAs.
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Rodentia;
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(La ribonucleoprotein)
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Pfam; PF05383; Pfam; PF00076;

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InterPro; [nterPro;

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Best Local
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P38656;
01-FEB-1995
01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
RNA-binding; Nuclear Protein; Phosphorylation.
RNA-BINDING (RRM)
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the EMropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sentities.com/license/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/see/filense/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sgreement/sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation of rat cDNA clones coding for the detection of species-specific variations."; Gene 126:265-268(1993)
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Pfam; PF00076; rrm; 1
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InterPro; IPR006630; Lupus La_dom
InterPro; IPR000504; RNA_rec_mot.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bachmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Semsei I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             v
                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Interacts with DDX15 (By similarity):
SUBCELLULAR LOCATION: Nuclear (Probable)
PYM: Phosphorylated (By similarity):
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.55, 55, 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                            of RNA polymerase III transcripts including tRNA and 7-2 RNAs.
                                                             JC1494; JC1494.
rPro; IPR002344; Lupus_La.
rPro; IPR006630; Lupus_La_dom
rPro; IPR000504; RNA_rec_mot.
                                                                                                                                                      X67859; CAA48043.1;
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(Rel.
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66.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                                                                                                                                                                                                                    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce,
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TISSUE-Placenta, and Skeletal muscle;

RC TISSUE-Placenta, and Skeletal muscle;

RX MEDLINE-2388257; PubMed=12477932;

RX MEDLINE-2388257; PubMed=12477932;

RX Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Hopkins R.F., Jordan H., Morre T.A., Rubin G.M., Hong L.,

RX Lapleton M., Marin R., Farmer A.A., Rubin G.M., Hong L.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Albastin M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RX RAha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RX Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Mitting M., Touchman J.W., Green E.D., Dickson M.C.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX Butterfield Y.S.N., Krzywinski M.J., Shalska U., Smailus D.E.,

"Generation and mouse CDNA sequences.";

Promote T. Touch Control of The Promote CDNA sequences.";
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89053970; PubMed=3192525; Chambers J.C., Kenan D., Martin B "Genomic structure and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89202037; PubM
Chan E.K.L., Sullivan
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Mammalia; Eutheria;
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ribonucleoprotein)
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15-MAR-2004
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                                                                                            Gottlieb E., Steitz J.A.;
"Function of the mammalian La
transcription termination by F
EMBO J. 8:851-861(1989).
                                                                                                                                                                                                                                                                                                     Chambers J.C., "Isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sturgess A.D., Peterson M.G., Coppel R.S.;
                        PHOSPHORYLATION.
MEDLINE=97207017;
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                                                                                                                                                                                                                                                                                      antigen
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н.,
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004 (Rel. 43, Last annotation update)
protein (Sjogren syndrome type B antigen)
                                                                                                                                                                                                                                                                                                                                                                                   54-97
                                                                                                                                                                                                                                                              Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                 140:3212-3218(1988).
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Res. 17:2233-
                                                                                                                                                                                                                                                                                                          Keene J.D.; analysis of cDNA clones expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263:18043-18051(1988)
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PubMed=2468131;
ivan K.F., Tan E.M.;
                          PubMed=9054510;
                                                                                                                                                                                                                                                              Sci.
                                                                                                                                                                                                                                                                                                                                                          PubMed=3856888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci.
                                                                                                                                                                                         PubMed=2470590;
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Primates;
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                              82:2115-2119(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99:16899-16903 (2002)
    J.L.,
                                                                                                                       polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Prange C.,
, Mullahy S.J.,
naratne P.H.,
J., Hulyk S.W.,
       Maraie
                                                                                                                                                  action
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Best Local
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RNA 8:1428-1443/2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC020818;
PIR; A31888; A31
Genew; HGNC:1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recycling of RNA polymerase Cell 88:707-715(1997).
                                                                                                                                                                     DOMAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0000 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                    PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
Systemic lupus erythematosus; R
Nuclear protein.
                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002344;
InterPro; IPR006630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO:0003729;
GO:0000049;
GO:0008334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-TERMINAL PART OF THE PROTEIN.

PYM: The N-terminus is blocked.

DISEASE: Sera from patients with systemic lup often contain antibodies that react with the La protein as if this antigen was foreign.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PHOSPHORYLATED. THE PHOSPHORYLATION C-TERMINAL PART OF THE PROTEIN.
PTM: The N-rerminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 7-2 RNAs.
SUBUNIT: Interacts will
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 RNA recognition motif (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0006400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0030529;
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                                                                                                                                                                                                                                                                                                                                                                                                              PF05383; La; 1
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BC020818; AAH20818.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X13697; CAA31985.1;
14
                                                                                                                                                                                                                                                                                                                           SM00360;
                                          N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:11316; SSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                         Similarity
EAKICHQIEYYFGDF
                                        ERAIIRQVEYYFGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000504;
                                                                                                                                                                       408
                                                                                    Conservative
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                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:ribonucleoprotein complex
F:mRNA binding; TAS.
F:tRNA binding; TAS.
F:tRNA mRNA metabolism;
P:tRNA modification; TAS.
                                                                                                                                                                                                                                                                                                                           RRM;
                                                                                                                                                                                           187
366
                                                                                                                                                                                                                                                                                                                                                                                                                             Lupus_La.
Lupus_La_dom.
RNA_rec_mot.
                                                                                                                                                                       46837
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                                                                                                                                                                                                                                                                                                                                                                                                                           RNA_rec
                                                                                                         67.9%;
66.7%;
  28
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                                                                                                      Score
Pred.
                                                                                                                                                                     RNA-BINDING (RRM).
PHOSPHORYLATION (B)
; EC153C15F9187FC4
                                                                                                                                                                                                                                                            RNA-binding; Phosphorylation;
                                                                                       Mismatches
                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex;
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                                                                                           DB .
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                                                                                                                             Length 408,
                                                                                                                                                                         CRC64;
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5S, 7S,
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"The genome sequence of Drosophila melanogaster.";

"The genome sequence of Drosophila melanogaster.";

"C. -- FUNCTION: May be involved in transcription termination by RNA
                                                                            Query Match
Best Local S
Matches 15
                                                                                                                                                                                                FlyBase; FBgn0011638; La.
GO; GO:0008098; F:5S rRNA primary transcript binding; IDA
GO; GO:0003723; F:RNA binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003666; AAF53885.1; -. PIR; A53773; A53773. PIR; A53781; A53781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U07652; AAA20518.1; -. EMBL; L32988; AAA21776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glands.
SIMILARITY: Contains 1 RNA recognition motif (RRM)
SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo followed by a restricted pattern of mesodermal expression that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            later confined to the visceral mesoderm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymerase III. Binds RNA and DNA. Binds to precursors
polymerase III transcripts. May play a specialized rolo
50
                                      <u>س</u>
                                                                                                    Similarity
QERAIIRQVEYYFGD
                                QERAIIRQVEYYFGD 15
                                                                                                                                                           149
169
182
283
283
329
                                                                               Conservative
                                                                                                                                                                                 329
                                                                                                                                                              44884
                                                                                                100.0%;
                                                                                                                       92.9%;
64
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                                                                            0;
                                                                                                Score 78; DB 1;
Pred. No. 3.9e-C
                                                                                                                                                                               A -> R (IN REF. 1).
K -> N (IN REF. 1).
                                                                                                                                                                                                                   RNA-BINDING (RRM).
A -> T (IN REF. 1).
KH -> NS (IN REF. 1).
                                                                                                                                                                                                                                                                                 DNA-binding.
                                                                                                                                                              A8099288B90446A5 CRC64;
                                                                               Mismatches
                                                                            3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermal expression that is gonads, gut, and salivary
                                                                                                                     Length 390;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    role during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by RNA
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P10881;
01-JUL-1989
01-JUL-1989
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences for RNA-binding."

Nucleic Acids Res. 17:2233-2244(1989).

Nucleic Acids Res. 17:2233-224 (1989).

I polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation
DOMAIN 111 187 RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chan E.K.L., Sullivan K.F., Tan E.P. "Ribonucleoprotein SS-B/La belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13698; CAA31986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89202037;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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SUBCELULAR LOCATION: Nuclear (Probable).
PIM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES
C-TERMINAL PART OF THE PROTEIN.
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                                                                                                                                                                                                                                        2 ERAIIRQVEYYFGDF
                                                                                                                                                                                                                                                                                                                        Similarity
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IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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; PubMed=2468131;
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Score
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84
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Copyright (c) 1993 - 2004 Compugen Ltd.
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7227; 7227; DM N.A. DM N.A. 19932; Tol 2., Tol 2., Tol 2., Tol biol. 109661; DM N.A. 199661; DOM N.A. 199661; Dolin S. 19661; Dolin S. 19661; Dolin S.	STAI 375; Q91 (Rel. (Rel. (Rel.) Comolog 22. 22. 22. 22. 22. 22. 22. 22. 22. 22	44444444444444444444444444444444444444
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vary; 8035794; 2035794; 2015 of a 2015 of a 2019 (1994). 5129 (1994). 5129 (1994).	ALIGNM PRT; ated) t sequence u t annotation bonucleoprot Fruit fly) pooda; Hexap Diptera; Bra e; Drosophil	POLG_FMDVI Y818_PYRAB YCDM_ECO57 YCDM_ECO57 YCDM_ECO51 SYR_MYCLE VP45_HUMAN VP45_MOUSE VP45_RAT VP45_RAT VP45_RAT VP45_RAT VP45_RAT CP45_SULTOO GUNH_CLOTM CHO2_SCHPO
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binding protein -associated romyces	tigen homolog). terygota; orpha;	P03310 foot-and-mo Q8zyel pyrobaculum Q8xaul escherichia P75898 escherichia P45840 mycobacteri Q9nrw7 homo sapien P97390 mus musculu Q08700 rattus norv Q03498 plasmodium Q974n6 sulfolobus P16218 clostridium Q974787 schizosacch
	NCBI_TaxID=7227; [1]	DROME LA DROME LA DROME LA DROME LA DROME STANDARD; PRT; 390 AA. P40796; Q24375; Q9VIN2; 01-FEB-1995 (Rel. 31, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 15-MAR-2004 (Rel. 43, Last annotation update) 16-DROME LA DROME LA DROME LA Protein homolog (La ribonucleoprotein) (La autoantigen homolog). LA OR CG10922. Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Reptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Reptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Reptera; Endopterygota; Drosophila. NCBI TaxID=7227; 11 SEQUENCE FROM N.A. STRAIN=Canton-S; TISSUE=Ovary; MEDLINE=94399632; PubMed=8035794; Bai C., Li Z., Tolias P.P.; Bai C.,

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A;Title: Isolation, characterization, and expression in Escherichia coli of a cDNA encod A;Reference number: A35199; MUID:90237051; PMID:2185251
A;Accession: A35199
A;Molecule type: mRNA
A;Residues: 1-315 <ROT>
A;Residues: 1-315 <ROT>
A;Cross-references: GB:J05405; NID:g204626; PIDN:AAA41340.1; PID:g204627
A;Cross-references: M.D.
J. Biol. Chem. 263, 3348-3353, 1988
A;Title: Evidence suggesting that the two forms of heme oxygenase are products of differ A;Reference number: A29922; MUID:88139412; PMID:3343248
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S19365
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A; Residues: 'EFRNK', 147-229, 'TEF' <CRU's
A; Cross-references: GB:M18918; NID:g204649;
C; Superfamily: heme oxygenase (decyclizing)
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                   A;Gene: SGD:SRO9
A;Cross-references: SGD:S0000542; MIPS:YCL037c
A;Map position: 3L
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Search completed: September 10, 2004, 18:02:42 Job time : 15.514 secs
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Best Local Similarity
Thes 7; Conserva
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C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
C;Accession: S13365
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A;Residues: 1-466 <DEL>
A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42379.1; PID:g5326; MIPS:YCL037c
                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Delgado, M.; Esteban, M.; Navas, L. submitted to the Protein Sequence Database, March 1992
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Local Similarity 40.0%;
hes 6; Conservative
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Pred. No. 14;
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A;Status: pre......
A;Molecule type: DNA
A;Residues: 1-298 <BAD>
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R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence. A;Reference number: Z14180
A;Accession: T00677
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T38937
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A;Reference number: A84420; MUID:20083487; PMID:10617197
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein At2g43970 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F6E13.10 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #se
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A;Reference number Z21818
A;Accession: T38937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rna binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Map position: 2
A;Introns: 200/3; 228/1; 25
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A; Residues: 1-529 < ROU>
RNA-binding
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A; Residues: 1-529 <STO>
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Experimental source: cultivar Columbia
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7; Conserv
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8; Conserv
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llarity 72.7%;
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1; Mismatches
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;Date: 01-Dec-2000
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heme oxygenase (decyclizing) (EC 1.14.99.3) 2 [similarity] - C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_chan C;Accession: A35199; A29922 R;Rotenberg_M.O.; Maines, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Recession: H83743
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C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43542; T43325
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-642 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04471.1;
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-298 <UTS>
A;Cross-references: EMBL:AB011371; PIDN:BAA24981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: the binding of the La protein to tRNA precursors C;Keywords: phosphoprotein; RNA binding
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Pred. No.
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein re
C;Keywords: phosphoprotein; RNA binding
F;112-178/Domain: ribonucleoprotein repeat homology <RRM:
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                                                                                                                                                             R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G. J. Mol. Biol. 231, 196-204, 1993
A;Title: La proteins from Xenopus laevis. cDNA cloning and A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33817
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C; Superfamily: 1
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A;Experimental source: strain Bristol N2; clone C44E4
C;Genetics:
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                                                             ay act as a transcription termination factor. C; Superfamily: ribonucleoprotein La; ribonucleoprotein repeat
                                                                                              A;Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876 C;Comment: This protein associates with a variety of small RNA molecules
                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-427 < SCH >
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A; Residues: 1-396 <S
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                                               C; Keywords: phosphoprotein; RNA binding
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;151-158/Region:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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               112-117/Region:
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les 8; Conserv
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Wohldmann, P.; Gillam, B.
1999
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ribonucleoprotein repeat homology RNA-binding RNP2 motif RNA-binding RNP1 motif
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66.7%;
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Pred. No.
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Pred. No. 0.042;
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0.67;
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                                   <RRM>
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                                                                                                     molecules,
                                                                                                                                                                                                                                                                   22-Jun-1999
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     RESULT 10
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NAIternate names: autoantigen SS-B/La; ribonucleoprotein SS-B (Species: Xenopus laevis (African clawed frog) (C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change C;Accession: S33818; S28545
R,Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
A,Title: La proteins from Xenopus laevis. cDNA cloning and devel A;Reference number: S33817; MUID:93287095; PMID:8510143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;112-178/Domain: ribonucleoprotein repeat homology F;113-118/Region: RNA-binding RNP2 motif F;151-158/Region: RNA-binding RNP1 motif F;228-428/Domain: phosphorylated #status predicted <
                                                                                                                                                                                                                                                                                                                                              R; Bevan, M.; Benes, V.; Rechmann, submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F4D11.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: ribonucleoprotein La; ril
C; Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715 C;Comment: This protein associates with a variety of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-428 < SCH>
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                                                                                                                                                   A; Map position: A; Introns: 17/3; A; Note: F4D11.80
                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL022537
                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-483 <BEV>
                                                                                                                                                                                                                                                                                                         A; Reference number: Z15360
A; Accession: T04453
                                                                                                                                                                                                                                                                                                                                                                                    C;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                               A;Experimental source: cultivar Columbia; BAC clone F4D11
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Best Local S
Matches 8
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KTVLRQVEFYFSD 24
                                 RAIIRQVEYYFGD 15
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                                                                         Conservative
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                                                                                           57.1%;
53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                              S.; Borkova, D.; Ansorge, W.; Hoheisel, J.;
Database, April 1998
                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
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                                                                                                                                                                         206/2;
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                                                                           <u>ب</u>
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A;Accession: A31888
A;Accession: A91888
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-408 <CHA>
A;Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687
A;Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687
A;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with cons
A;Reference number: S03848; MUID:89202037; PMID:2468131
A;Accession: S03848
A;Accession: S03848
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C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: Al1888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; R;Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.
R;Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A;Title: Genomic structure and amino acid sequence domains of the human La at A;Reference number: A31888; MUID:89053970; PMID:3192525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: This protein associates with a variety of small RNA molecules,
ay act as a transcription termination factor.
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: blocked amino end; phosphoprotein; RNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Ribonucleoprotein SS-B/La belongs to a protein A; Reference number: S03848; MUID:89202037; PMID:2468131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989
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                                                    R;Chambers, J.C.; Keene, J.D.
Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDNA clones expressing human A;Reference number: A22956; MUID:85166283; PMID:3856888
A;Accession: A22956
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A; Molecule type: mRNA
A; Residues: 45-97, 'LK'
                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-408 <CH2>
A;Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1; PID:g36415
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Best Local S
Matches 10
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Matches 15; Conserv
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:151-158/Region: RNA-binding RNP1 motif
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A,Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457 R;Kohaaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka, J. Clin. Invest. 85, 1566-1574, 1990 A;Title: Fine epitope mapping the human SS-B/La protein: Identification of A;Reference number: I55553; MUID:90237237; PMID:1692037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-19, 'E', 21-47 <NYM>
R;Sturgess, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, J. Immunol. 140, 3212-3218, 1988
A;Title: Characteristics and epitope mapping of a cloned human A;Reference number: S11013; MUID:88199081; PMID:2452201
A;Accession: S11013
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                                                                                                                                                                                                                                                                                                                        RESULT
JC1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;113-118/Region: RNA-binding RNP2 motif
F;151-158/Region: RNA-binding RNP1 motif
F;228-408/Domain: phosphorylated #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 279-342 <RE3>
A;Crooss-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
C;Comment: This protein associates with a variety of small RNA molecules,
                                                                         R;Semsei, I.; Troester, H.; Bartsch, H.; Schwemmle, M.; Igloi, G.L.; Bachmann, Gene 126, 265-268, 1993
A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Dete A;Reference number: JC1494; MUID:93246255; PMID:7916708
                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: JC1494; S25145
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A; Residues: 174-224 < RE2 >
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A; Residues: 81-107 < RES>
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A;Residues: 'E',55-287,'V',289-408 <STU>
                                               A;Reference number:
A;Accession: JC1494
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;Molecule type: mRNA
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Pred. No. 0.041;
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ALIGNMENTS

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C;Accession: A53781
R;Yoo, C.J.; Wolin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast
A;Reference number: A53781; MUID:94309661; PMID:8035818
A;Accession: A53781
                                                                                                                                                                                                                                                                                                                                                                                          ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: leucine zipper; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Bai, C.; Li, Z.; Tolias, P.P.
Mol. Cell. Biol. 14, 5123-5129, 1994
A;Title: Developmental characterization of
A;Reference number: A53773; MUID:94309632;
A;Accession: A53773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  La/SS-B homolog D-la - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: A53773
                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-390 <YOO>
A;Cross-references: GB:L32988; NID:g488469; PID:g488470
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A;Residues: 1-390 <BAI>
A;Cross-references: GB:
                                                                   A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; ri
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Matches
                                           Keywords: RNA binding
Query Match
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92.9%;
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  Score
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                                                                      ribonucleoprotein repeat homology
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  78;
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8e-06;
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  Length 390;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylglucosamine pyrophosphorylase.

PRELIMINARY;

PRT;

451 AA

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RESULT 15
004697
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Matches 8; Conserv
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InterPro; IPR001451; Hexappp_transf.
InterPro; IPR001451; Hexappp_transf.
InterPro; IPR005835; NTP_transferase.
Pfam; PF00132; hexappp; 6.
Pfam; PF00483; NTP_transferase; 1.
TIGRFAMs; TIGR01173; glmU; 1.
Complete proteome.
SEQUENCE 451 AA; 49191 MW; BIDEB3A6
                                                              SEQUENCE FROM N.A.

SETRAIN=cv. Alaska; TISSUE=Leaf;
Sato N., Kazuno A.A., Ohta N., Ohshima K.;
Sato N., Kazuno G.A., Ohta N., Ohshima K.;
Sato N., Kazuno A.A., Ohta N., Ohshima K.;
"Identification of a novel family of DNA-binding proteins with hook motifs from pea.";
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X99740; CAA67292.1; -.
EMBL; X99740; CAA67292.1; -.
PIR; T06586; T06586.
GO; GO:0003677; F:DNA binding; IEA.
DNA-binding.
SEQUENCE 632 AA; 69498 MW; 9F744E227CD08717 CRC64;
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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Pisum sativum (Garden pea).

Pisum sativum (Garden pea).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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01-JUL-1997 (TrEMBLrel. 04,
01-OCT-2003 (TrEMBLrel. 25,
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Pred. No. 65;
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Pred. No.
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Muraki A.,
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Search completed: September 10, Job time: 44.229 secs 2004, 18:00:17

SMART; SM00192; SMART; SM00220; SMART; SM00219;

S_TKC; 1. TyrKc; 1.

ProDom;

PD000001; Prot

kinase;

LDLa;

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RESULT
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DT 01
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 Q8PXT9;
01-OCT-2002
01-OCT-2002
01-JUN-2003
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosomal-protein-alanine N-acetyltransferase (EC 2
RIMI1 OR LP_0718.
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SEQUENCE
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PROSITE; PS50068; LDLRA_2; 1.

PROSITE; PS00107; PROTEIN KINASE DOM;
PROSITE; PS0011; PROTEIN KINASE DOM;
PROSITE; PS00109; PROTEIN KINASE TYR;
PROSITE; PS00239; RECEPTOR TYR_KIN_II;
                                                                                                                                                                                                                                                                                                                                        STRAIN-NCIMB 8826 / WCFS1;
MEDLINE-22480296; PubMed=12566566;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molena Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbr Fiers M.W.E.J., Stlekema W., Klein Lankhorst R.M., Bron Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries De Vos W.M., Siezen R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QB8YN2;
01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                Q8PXT9
                                                                                                                                                                                                                                                        "Complete genome sequence of Lactobacillus plantarum WCFS1."; proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).

EMBL; AL93523; CAD63319.1; -.

GO; GO:0008415; F:acyltransferase activity; IEA.

GO; GO:000880; F:N-acetyltransferase activity; IEA.

GO; GO:0008999; F:ribosomal-protein-alanine N-acetyltransfera.

GO; GO:0016740; F:transferase activity; IEA.
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Bacteria; Firmicutes; La
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pfam; PF00583; Acetyltransf; 1.
Acyltransferase; Complete
SEQUENCE 160 AA; 18734 MW; 3FD1115
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llarity 53.8%;
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Pred. No. 1.5e
4; Mismatches
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Q86119;
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"The genome of Methanosarcina mazei: evidence for lateral g
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STRAIN=Goel / Gol / ATCC BAA-199 /
MEDLINE=22120827; PubMed=12125824;
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GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001173; Glyco trans 2.
Pfam; PF00535; Glycos transf_2; 1.
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                                                                                                                                                                          Submitted (MAR-2003) to the EMBL; AC117176; AAO52103.1; Hypothetical protein. SEQUENCE 358 AA; 39920 MW
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Gloeckner G., Elchinger L., Szafranski K., Pachebat J., Dear P.,
Gloeckner G., Blochinger C., Parra G., April J.F., Guigo R., Kumpf K.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
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Dictyostelium discoideum (Slime
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GO; GO:0006535; P:cysteine biosynthesis fro
GO; GO:0019343; P:cysteine biosynthesis via
InterPro; IPR001926; B6 enzyme beta.
InterPro; IPR001926; B6 enzyme beta.
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InterPro; IPR001216; Cys_synthase_BS.
Pfam; PF00571; CBS; 2.
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Pfam; PF04330; DUF484; 1.
Hypothetical protein; Complete
Hypothetical protein; 24078 MW;
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C. Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Meyer T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathavan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wamathavan J., Weidman J., Uterback T.R., McDonald L.A., Fraser C.M.; Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015863; AAN57276.1; -.
TIGR; SO4307; -.
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Best Local S
Matches 10
                                                                                                                                      R EMBL; AL596022; CAD43463.1; -...

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:000474; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004714; F:transferase activity; IEA.

R GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. ...

R GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. ...

R GO; GO:0001638; P:protein amino acid phosphorylation; IEA.

R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ...

R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ...

R InterPro; IPR002172; LDL receptor_A.

R InterPro; IPR002173; Prot. kinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR001249; Tyr_pkinase.

R InterPro; IPR001265; Tyr_pkinase.
                          InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; RecepttyrkinsII.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase_AS.
Pfam; PF00057; Idl recept_a; 1.
Pfam; PF00069; pkinase; 1.
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PSS0102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
SEQUENCE 401 AA; 46138 MW; 2E
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Q8JFV0;
01-OCT-2002
01-OCT-2002
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01-OCT-2003 (TREMBLrel. 25, Last sanoctation update)
5imilar to sjogren syndrome antigen B (Autoantigen La).
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rotinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SI:dCI07016.1 (Novel protein similar to vertebrate anaplastic lymphoma kinase (ALK) and leukocyte tyrosine kinase receptor prescursor (LTK or TYK1)) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hammond S.;
Submitted (AUG-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SI:DZ107016.1.
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EMBL; BC045392; Ah445392.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding;
CO; GO:00037244; Lupus_La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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Pred. No. 46
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Best Local S
Matches 11
                                                                    Query Match
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Chen Z., Wen Y.;
Submitted (NOV-2002) to the EMBL/
EMBL; AE016750; AA005481.1; -.
Hypothetical protein; Complete pu
SEQUENCE 116 AA; 14002 MW; Ci
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01-JUN-2001
01-OCT-2003
                                                                                                                                                                       EMBL; AK017822; BAB30957.1; -. MGD; MGI:98423; Ssb. GO; GO:0005634; C:nucleus; IDA. InterPro; IPR005344; Lupus La. InterPro; IPR006630; Lupus La_dom. InterPro; IPR000504; RNA_rec_mot.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=ATCC 12228;
                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690\,(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                           SEQUENCE
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                                                                                                                                                                Pfam; PF05383; La; 1.
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SM00715; LA;
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                          VSKLEASTIRQ-EYYFGD
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Pred. No. 7.
                                                                                Score 43.5;
                                                                    Pred. No.
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Sciurognathi; Muridae;
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C8419BFA9B8A7EA5 CRC64;
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; Murinae; Mus.
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Best Local S
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1
SEQUENCE 415 AA; 47657 M
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01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:98423; Ssb. GO; GO;005534; C:nucleus; IDA. interPro; IPR002344; Lupus_La_dom. InterPro; IPR006501; Lupus_La_dom. InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FANTOM Consortium, the RIKEN Genome Exploration Research transcriptome "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
ASBC Journal 50:130-133(1992).

EMBL; D16496; BAA03947.1; -.

HSSP; P35520; JJBQ.

G0; G0:0005737; C:cytoplasm; IEA.

G0; G0:0004122; F:cystathionine beta-synthase

G0; G0:0016829; F:lyase activity; IEA.
                                                                 STRAIN-X2180-1A; rezuka H., Mori T., Okumura Y., Kitabatake K., Tsumura Y.; rezuka H., Mori T., Okumura Y., Kitabatake K., Tsumura Y.; rCloning of a gene suppression huydrogen sulfide production by saccharomyces cerevisiae and its expression in a brewing yeast.";
                                                                                                                                                                                                                                                         094073
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01-OCT-2003
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                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                  Cystathionine
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local S
Matches 12
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01-MAY-2000
01-MAY-2000
01-JUN-2003
CG12014 prot
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01-OCT-2003 (TrEMBLrel.
Hypothetical protein.
F25G13.200 OR AT4G13110.
                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL079349; CAB45510.1; -.
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Mayer K.F.X., Lemcke K., Schueller
Submitted (JUN-1999) to the EMBL/Ge
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01-MAY-2000
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InterPro; IPR005607; BSD.
Pfam; PF03909; BSD; 1.
PROSITE; PS50858; BSD; 1.
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                                                                                                                                                           Drosophila melanogaster (Fruit fly).
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bmitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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hueller C.;
EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation updat
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Pred. No. 0.67;
2; Mismatches
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                                                                                             ecta; Pterygota;
Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 365;
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RESULT 4
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RA Bescon K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA de Pablos B., Del.Cher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Del.Cher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A. E., Garg N. S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A. E., Garg N. S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T. J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Mount S.M., Molson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun S.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Chibs R.A., Myers B.W., Rubin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.";
L. Science 287:2185-2195(2000).
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                                                                                         Staphylococcus epider
Bacteria; Firmicutes;
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                                                                                                                                                                                     Conserved hypothetical protein.
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1: sp_archea:*
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SUMMARIES
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Q9HCL3;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chee M.S., Bankier A.T., Beck S. Bohni R., Brown C.M., Cerny R., Horsmell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G., "Analysis of the protein-coding content of the sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P16818;
                        XVIII. The complete sequences of 100 new cDNA code for large proteins in vitro."; DARA Res. 7:273-281(2000).

-i- FUNCTION: May function as a transcription-i- SUBCELLULAR LOCATION: Nuclear (Probable).

-i- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY
                                                                                             MEDLINE=20450683; PubMed=10997877;
Nagase T., Kikuno R., Nakayama M., Hirosawa M., Chara O.;
"Prediction of the coding sequences of unidentified human
XVIII. The complete sequences of 100 new cDNA clones from
                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
<del>-</del>
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SIMILARITY: Contains 1 KRAB domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EASTIRQEYYFGDA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 15, Last & (Rel. 17, Last & 1 protein UL61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 15, Created)
(Rel. 15, Last seq
(Rel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S09824.
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                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                   41, Created)
41, Last sequence update)
42, Last annotation update)
finger protein KIAA1559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44309 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.3%;
                                                                          in vitro.";
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annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB
Pred. No. 34;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61CC7288FA3B0743 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AA
                                                                                                                                                                                                                                                                                                                                          533
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                             FAMILY OF
                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Length 431;
                                                       factor.
                             C2H2-TYPE ZINC
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EMBL outstation -
                                                                                                 genes.
brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Search completed: 9
Job time : 9.24022
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                                                                                             Matches
                                                                                                                  Query Match
                                                                                                                                                     ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01352; KRAB; 1. Pfam; PF00096; zf-C2H2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50805; KRAB; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 13.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P25490; 1UBD.
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                     Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 13 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001909;
InterPro; IPR007087;
                                                                                                        Local
                                               127
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB046779;
                                                                     N
                                                                                            Similarity
8; Conserv
                                               SKIEGEKEQQEGYFG
                                                                      SKLEASTIRQEYYFG
                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                     protein; Transcription regulation; DNA-binding; Metal-binding; Nuclear protein; Repeat.
  September
2 secs
                                                                                                                                            A.
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                                                                                                        43.3%;
53.3%;
                                                                                                                                             63463
                                                                                                                                                                                                                                                                                                                                                                                                                       znf_C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          KRAB.
             10,
                                                                     16
                                                141
                                                                                                                                            MW.
            2004, 17:53:12
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                                                                                                                                                      C2H2-TYPE
C2H2-TYPE
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C2H2-TYPE
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C2H2-TYPE
C2H2-TYPE
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C2H2-TYPE
                                                                                                                                                                                                                                                                                    C2H2-TYPE
                                                                                                                   Score 39;
                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                            KRAB.
                                                                                                                                             E40EF5EC22A99F10 CRC64;
                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                        13.
                                                                                                           42;
                                                                                                                                                                              10.
                                                                                                                      BB
                                                                                                                    1:
                                                                                              <u>.</u>
                                                                                                                    Length 533;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
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RESULT 12
SYA_STAAW
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Best Local S
Matches 8
     Query
Best I
                                                                                                                                                                                                                                    EMBL; AP004827; BAB95433.1; -.
HAMAP; MF 00038; -; 1.
InterPro; IPR003156; DHHA1.
InterPro; IPR002318; tRNA-synt_2c.
InterPro; IPR006193; tRNA synt_Ala.
Pfam; PF02772; DHHA1; 1.
Pfam; PF01411; tRNA-synt_2c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00036; -; 1.
InterPro; IPR003156; DHHA1.
InterPro; IPR003188; tRNA-synt 2c.
InterPro; IPR006193; tRNA_synt_Ala.
Pfam; PF02272; DHHA1; 1.
Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYA_STAAW
Q8NW87;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                 Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; Complete proteome.
SEQUENCE 876 AA; 98505 MW; 5D9D662D8DDAEDFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagai Y., Iwama N., Asano K., Naimi T., Kuroqa H., Cui L., Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-
                                                                                                                                                        PRINTS; PR00980; TRNASYNTHALA.
TIGREAMS; TIGR00344; alaS; 1.
PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=22040717; PubMed=12044378;

Baba T., Takeuchi F., Kurdda M., Y.

Tanan K. Naman K. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amotation updat
Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanir
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 359:1819-1827(2002).
-!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 876 AA;
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PROSITE; PS50860; AA_TRNA_LIGASE_II_ALA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acquired MRSA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding,
     Local Similarity
                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diphosphate + L-alanyl-tRNA(Ala).
SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A89944; A89944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 61.5
8; Conservative
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61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement
     44.4%;
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Pred. No. 48;
3; Mismatches
     Score
Pred.
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        No ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n update)
(Alanine--tRNA ligase) (AlaRS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
DB
48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H., Aoki K.-I., Oguchi A.,
Kuroda H., Cui L.,
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                             Length 876
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                                                                                                                                  ATP-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                      Matches
                                                                                                                                  Best
                                                                                                                                                     Query Match
                                                                                                                                                                                         InterPro; if volume is a substitution of the pfam; PF00185; OTCace, 1.

Pfam; PF02729; OTCace, N; 1.

PRINTS; PR00100; AOTCAGE.

TIGRAMS; TIGR00670; AGE Carb tr; 1.

TIGRFAMS; TIGR00670; CARBANOYLTRANSFERASE; 1.

PROSITE; PS00097; CARBANOYLTRANSFERASE; Complete p
Pyrimidine biosynthesis; Transferase; Complete p
Pyrimidine biosynthesis; Transferase; Complete p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRB_DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00001; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00479; 3CSU.
TIGR; DR1109; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001961; AAF10682.1; PIR; D75435; D75435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcarbamylase) (ATCase).
PYRB OR DR1109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PATHWAY: Pyrimidine biosynthesis; second step.-!- SIMILARITY: Belongs to the ATCase/OTCase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Deinococcus-Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [nterPro;
                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        + N-carbamoyl-L-aspartate.
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148
                                               4
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IPR002082; Asp_carbmltransf.
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IPR006132; OTCace_P.
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                                                                 EMBL; M74453; AAA35230.1; -.
EMBL; X60326; CAA42896.1; -.
EMBL; X92517; CAA63285.1; -.
EMBL; Z71430; CA396041.1; -.
PIR; S29522; S29522.
HSSP; P40233; ICSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang P.-C., Vancura A., Mitcheson T.G.M., "Two genes in Saccharomyces cerevisiae encof casein kinase-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=5288C;
STRAIN=5288C;
MEDLINE=92108037; PubMed=1729698;
MEDLINE=92108037; PubMed=1729698;
MEDLINE=92108037; PubMed=1729698;
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YCK2 OR CKI1 OR
                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roach P.J., Kung C., Haas D.W., Hagedorn C.H. Culbertson M.R., Carlson M.; "Yeast casein kinase I homologues: an essentiproc. Natl. Acad. Sci. U.S.A. 89:28-32(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991
10-OCT-2003
                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nasr F., Becam A.-M., Herbort C.J.;
"The sequence of 36.8 kb from the left arm of chromosome XIV reveals 24 complete open reading frames: 18 correspond to new genes, one of which encodes a protein similar to the human myotonic dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                     GermOnline;
                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase.
 ; S0005098; YCK2.
GO:0005935; C:bud neck; IDA.
GO:0005886; C:plasma membrane;
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SUBCELLULAR LOCATION: Plasma membrane-bound SIMILARITY: Belongs to the Ser/Thr family o Casein kinase I subfamily.
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se I homolog 2 (EC 2.7.1.-).
1 OR YNL154C OR N1755.
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encode a membrane-bound
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Goebl M.,
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NP_BIND
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                      aureus ";
Lancet 5;
Lancet 5;
Lancet 7; 1225-1240 (2001).
Lancet 7; 125-1240 (2001).
Lancet 7; 125-124
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MUSO / ATCC 700699, and N315;

STRAIN=MUSO / ATCC 700699, and N315;

MEDLINB=21311952; PubMed=114.8146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Kuroda M., Ohta T., Uchiyama I., Baba T., Lian J.-Q., Ito T.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabbuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., S

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Creat
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Alanyl-trNA synthetase (EC
ALAS OR SAV1618 OR SA1446.
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ProDom; PD000001; Prot kinase;
PROSITE; PS00107; PROTEIN_KINAS
EMBL;
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or send a
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE TOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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InterPro; IPR008271; Ser_
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                                                                                                                                                                                                                                                                                                                                                           "Whole genome sequencing of meticillin-resistant
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Bacteria; Firmicutes; Bacillales;
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GO:0000902;
GO:0000910;
GO:0006897;
GO:0006468;
                                                                                                                                                                                                                                         SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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AP003362;
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                                                                 an email to license@isb-sib.ch).
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hu50 / ATCC 700699, and N315;
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  BAB57780.1;
BAB42710.1;
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EMBL; X72922; CAA51426.1; -. EMBL; D16502; BAA03952.1; -. EMBL; X65807; CAA59812.1; -. EMBL; Z72940; CAA97169.1; -. EMBL; L14578; AA037401.1; -. PIR; A48661; A48661.
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-X2180-14;
MEDLINE-93374830; PubMed-8366024;
Cherest H., Thomas D., Surdin-Kerjan Y.;
"Cysteine biosynthesis in Saccharomyces (
"Cysteine hiosynthesis in Saccharomyces (
                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 structural and functional conservation of the human an Proc. Natl. Acad. Sci. U.S.A. 91:6614-6618(1994).
-!-CATALYTIC ACTIVITY: L-serine + L-homonvaroinal uron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skala J., Nawrocki A., Goffeau A.;
"The sequence of a 27 kb segment on the right arm of chromosome from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, PEMI/CHO2, NSR1 genes and ten new open reading frames.";
Yeast 11:1421-1427(1995).
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cystathionine beta-synthase (EC 4.2.1.22) (Serine sulfhydrase) (Beta-thionase).
CYS4 OR STR4 OR YGR155W OR G6667.
             SGD; S0003397; CYS4.

GG; GO:0005737; C:cytoplasm; IDA.

GG; GO:0004122; F:cystathionine beta-synthase activity;

GG; GO:0004124; P:cysteine biosynthesis; IMP.

InterPro; IPR001926; B6 enzyme beta.

InterPro; IPR001924; CB5_domain.

InterPro; IPR001216; Cys_synthase_BS.

InterPro; IPR001216; Cys_synthase_BS.

InterPro; IPR00557; Cysta_beta_synth.

Pfam; PF00571; CBS; 2.

Pfam; PF00291; PALP; 1.
                                                                                                                                                     GermOnline; 141467; -. SGD; S0003387; CYS4.
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                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
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STRAIN=S288c;
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)) to the
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e EMBL/GenBank/DDBJ databases.
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Matches 10
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BINDING
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030321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARCFU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical AF2348.
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                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                            reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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Archaeoglobaceae; Archae
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16-OCT-2001
                                         TIGR; AF2348; -.
                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                           Venter J.C.
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                                                                                                                                                                Usage,
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STRAIN=FVB/N; TISSUE=Mammary gland; MEDLINE=22388257; PubMed=12477932;

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A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

A Stapleton M., Galin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Małek J.A., Gunarathe P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Paley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Halkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Scherch A., Schein J.E., Jones S.J.
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Matches 10
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus_La_dom.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Groelz D., Bachmann M.;

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor: Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor form
of RNA polymerase III transcripts including tRNA and 4.58, 58, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                     PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
DOMAIN 111 187 RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Frobable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC003820; AAH03820.1; -. Y07951; CAA69249.1; -.
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10
                                                                                                      . Similarity
MTALEAKICHQIEYYFGD
                                             VSKLEASTIRQ-EYYFGD
                                                                                                                                                                                                               415 AA;
                                                                                                      Conservative
                                                                                                                                                                                                               47756 MW;
                                                                                                                            48.3%;
  27
                                                   17
                                                                                                                                                                                                             RNA-BINDING (RRM).
; 2D75197692FDC933 CRC64;
                                                                                                                              Score 43.5;
Pred. No. 5
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                                                                                                         Mismatches
                                                                                                                                                         DB 1;
                                                                                                      5.
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RABBE

Q05177;

STANDARD;

PRT;

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Created)
Last sequence update)
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RESULT 8
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P38656;
01-FEB-1995
01-FEB-1995
28-FEB-2003
CBS YEAST
P32582; Q051
01-OCT-1993
01-OCT-1993
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50102; RRM, 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
RNA-binding; Nuclear protein; RNA-BINDING (RRM)
DOMAIN 111 167 RNA-BINDING (RRM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X67859; CAA48043.1; -. PIR; JC1494; JC1494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93246255; PubMed=7916708; 
3emsei I., Troester H., Bartsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002344;
InterPro; IPR006630;
InterPro; IPR000504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including them and a second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 7-2 RNAs.
SUBURIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 RNA recognition motif (RRM)
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                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                 VSKLEASTIRO-EYYFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                    415 AA; 47777 MW;
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55.6%;
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Pred. No. 5
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Sciurognathi; Muridae;
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RX MEDLINE=23388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Scheefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Haby J., Helton E., Kettenna M., Madan A., Rodrigues S., Sanchez A.,

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"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                putative DEAH-box RNA helicase."; RNA 8:1428-1443(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fouraux M.A., Kolkman M.J.M., Van der Heijden A. Van Venrooij W.J., Pruijn G.J.M.; "The human La (SS-B) autoantigen interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97207017; PubMed=9054510; Fran H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Maraie R.J.; "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes."; Cell 88:707-715(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gottlieb E., Steitz J.A.;
"Function of the mammalian La protein: evidence for its "Function of termination by RNA polymerase III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89251617;
Gottlieb E., Stei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85166283;
Chambers J.C., Kee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTERACTION WITH DDX15
SUBCELLULAR LOCATION: Nuclear (Probable) PTM: PHOSPHORYLATED. THE PHOSPHORYLATION C-TERMINAL PART OF THE PROTEIN.
                                                                                                                                                                                                                                                       FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S
                                                                                                                                                                                                    SUBUNIT: Interacts with DDX15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8:851-861(1989)
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                                                                                                                                                                                                                                       ·2 RNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acad.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDX15.
PubMed=12458796;
PubMed=1.45.0796;
Van der Heijden A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=3856888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2452201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=2470590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A. 82:2115-2119(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of cDNA clones expressing human lupus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L.J., Whittingham
                                                                                                                                        SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDX15/hPrp43,
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                                                                                                                                        ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jong A.S.,
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SO TIVE CONTRACTOR OF THE CONT
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Matches
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P32067;
01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Systemic lupus er
Nuclear protein.
DOMAIN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                      Topfer F., Gordon T., McCluskey J.;
Topfer F., Gordon T., McCluskey J.;
"Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and reartivity of recombinant protein with poly(U) and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 109090; -.

GO; GO:0030529; C:ribonucleoprotein complex; Ti
GO; GO:0003729; F:mRNA binding; TAS.
GO; GO:000049; F:tRNA binding; TAS.
GO; GO:00008334; P:histone mRNA metabolism; TAS.
GO; GO:0008334; P:tRNA modification; TAS.
                                                               reactivity of recombinant protein autoantibodies.";
                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00302; LUPUSL
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X13697; CAA31985.1; --
EMBL; J04205; AAA51885.1; --
EMBL; BC001289; AAH01289.1; --
EMBL; BC020818; AAH20818.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content
SEQUENCE
                                                                                                                                                                            MEDLINE=93203630;
                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                          SSB OR SS-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1
Systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
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                                                                                                                                                                                                                                                                                                                                                                                  Lupus La protein
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FROM N.A
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nilarity 55.6%;
Conservative
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(Rel.
(Rel.
                                            150:3091-3100(1993)
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                                                                                                                                                                                                                                                                                                                                                                    . 27, Created)
. 27, Last sequence update)
. 43, Last annotation update)
homolog (La ribonucleoprotein)
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                                                                                                                                                         PubMed=8454877;
T., McCluskey J
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366
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; RNA-binding; Phosphorylation;
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PHOSPHORYLATION (B)
; EC153C15F9187FC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43.5;
Pred. No. 5;
                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       autoantigen
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MBL outstation -
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RESULT 4
IA BOVIN
ID LA B
AC P108
AC P100-J
DT 01-J
DT 28-F
DE Lupu
DE Lupu
DE SSB.
OS Bos
OC Mamn
OC Bovi
OX NCBJ
RN [1]
RP SEQU
RZ MEDJ
RA Chaj
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RA Chaj
RT SEC
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CC -1-
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R HAMAP; MF 00127; -; 1.

R InterPro; IPR004154; HGTP_anticodon.

R InterPro; IPR004516; HisS.

R InterPro; IPR004516; HisS.

R InterPro; IPR006195; tRNA iggase II.

R Pfam; PF03129; HGTP_anticodon; 1.

R Pfam; PF03129; HGTP_anticodon; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LA BOVIN
P10881;
01-JUL-1989
01-JUL-1989
28-FEB-2003
                                                                                                                                                                                                                                                                     Mammalia;
Bovidae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MAFF303099;
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SEQUENCE FROM
                           TISSUE=Pituitary;

MEDLINE=89202037; PubMed=2468131;
Chan E.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
sequences for RNA-binding.";
Nucleic Acids Res. 17:2233-2244(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Lupus La protein homolog (La ribonucle
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                    homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                symiss-prot entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial statement is not removed. Usage by and specifications of the statement is not removed.
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CATALYTIC ACTIVITY: ATP + L-histidine +
diphosphate + L-histidyl-tRNA(His).
SUBUNIT: Homodimer (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteome
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                                                                                                                                                                                                                                                                                                                          Metazoa;
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                                                                                                                                                                                                                                                                                                                                                     (Bovine).
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  La protein plays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                           Bos.
                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54546 MW;
                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  st annotation update)
(La ribonucleoprotein) (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                  E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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Kawashima K., Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 AA.
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  transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 500;
                                                                                     family
                                                                                                                                                                                                                                                                                                 Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Sugimoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     autoantigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasamoto
                                                                                  with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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LA HUMAN TO LA HUM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS500030; RRM RNP_1; 1.
PROSITE; PS00030; RRM ENP_1; 1.
RNA-binding; Nuclear protein; Phopomain
autoantigen.";
J. Biol. Chem.
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LA HUMAN
P05455;
01-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as mot removed. and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                  MEDLINE=89202037; PubMed=2468131;
Chan E.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
sequences for RNA-binding ";
Nucleic Acids Res. 17:2233-2244(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Lupus La protein (Sjogren syndrome type B ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
                                                                                          MEDLINE=89053970; PubMed=3192525; Chambers J.C., Kenan D., Martin B
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribonucleoprotein (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X13698; CAA31986.1; -.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                  "Genomic structure and
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and 7-2 RNAs.
SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
SUBCELLULAR LOCATION: THE PHOSPHORYLATION SITES ARE AT THE PTM: PHOSPHORYLATED. THE PROTEIN.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor for of RNA polymerase III transcripts including tRNA and 4.5S, 5S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright: It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S03849; S03849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF05383; La; 1.
PF00076; rrm; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                          263:18043-18051(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (La autoantigen)
                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46534 MW;
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                                                                       amino
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                                                                       tin B.J.,
acid seq
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                       E.M.;
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                                                                     sequence
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                                                                                               Keene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions in as its content is in
                                                                                                                                                                                                                                  protein
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                                                                         domains
                                                                                               J.D.;
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                                                                                                                                                                                                                                    consensus
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5S, 7S,
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40 VSKLEASTIRQLEYYFGDA 58

RESULT 3 SYH_RHILO

Bacteria; Proteobacteria; Phyllobacteriaceae; Mesorl

Mesorhizobium

Alphaproteobacteria; Rhizobiales;

Rhizobium

(Mesorhizobium loti)

H RHILD

SYM RHILD

C Q987T0;

T 10-OCT-2003 (Rel. 42, Created)

T 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

T 10-OCT-2003 (Rel. 42, Last annotation update)

update)
(Histidine--tRNA ligase)

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RESULT

A COLUMN A CO
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., A., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Horil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Borkova D., Bocchan M.R., Bouck J., Broketein P., Brottier P.,
RA Burtis K.C., Blasam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Bocchan M.R., Bouck J., Broketein P., Brottier P.,
RA Burtis K.C., Blasam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bodson K., Doup L.B., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Ketchum K.A.,
RA Klamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mentalov G., Milshina N.V., Mobarry C., Morris J., Moshreil A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mentalov G.M., Strong R.C., Sthen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weinsenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Vang S., Yao Q.A.,
Pach J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DROME
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Canton-S; TISSUE=Ovary;
STRAIN=94309632; PubMed=8035794;
MEDLINE=94309632; PubMed=8035794;
MEDLINE=94309632; PubMed=8035794;
MEDLINE=94309632; PubMed=8035794;
MEDLINE=94309632; PubMed=8035794;
MEDLINE=94309632; PubMed=8035794;
MEDLINE=94309632; PubMed=8035794;
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P40796; Q24375; Q9VIN2;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
LA OR CG10922.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
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"Developmental characterization of a Dr
homologous to the human systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.J., Wolin S.L.;
proteins from Drosophila melanogaster and Saccharomyces
proteins a yeast homolog of the La autoantigen is dispens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoantigen."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14:5412-5424(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14:5123-5129(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10731132;
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
-!- FUNCTION: May be involved in transcription termination by RNA-
polymerase III. Binds RNA and DNA. Binds to precursors of RNA-
columnarase III transcripts. May play a specialized role during
                                                                                                                                                                                           CONFLICT
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PROSITE; PS00030; RRM_RNP_1; 1.
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Pfam; PF00076; rrm; 1
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PIR; A53781; A53781.
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SIMILARITY: Contains 1 RNA recognition motif (RRM)
SIMILARITY: TO VERTEBRATE PROTEIN LA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced thrown the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE003666; AAF53885.1; -.
48 TKQERAIIRQVEYYFGDA
                                                                                           l Similarity
12; Conser
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                              SKLEASTIRQ-EYYFGDA 18
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66.7%;
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Pred. No. 0.12
2; Mismatches
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RNA-BINDING (RRM).

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KH -> NS (IN REF.
                                                                                                                                                                                                                  A -> R (IN REF. 1).
K -> N (IN REF. 1).
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Run on:
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September 10, 2004, 17:01:41; Search time 7.24022 Seconds (without alignments) 129.452 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Title: Perfect score: US-09-836-073-18 90

Sequence: 1 VSKLEASTIRQEYYFGDA 18

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:*

Database :

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Query Match L	Length	B	ID	cription
1	79.5	88.3	383	<u>ب</u> ا	LA AEDAL	7
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6	43.5		415	щ		P32067 mus musculu
7	w	•	415	ш	LA RAT	P38656 rattus norv
80	43		507	_	CBS_YEAST	N
ø	40		112	μ	YN48 ARCFU	_
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11	40	٠	876	ᆫ	SYA_STAAM	_
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13	39	43.	314	1	PYRB_DEIRA	09rvc0 deinococcus
14	39	43.	431	ᆫ	UL61_HCMVA	
15	39	43.	533	-	YF59_HUMAN	ω
16	39	43.	550	Н	SYR_CORGL	-
17	39	43.	778	μ	SZ1B_BRARE	σ
18	39	43.	904	Н	SYA_SULTO	
19	38.5	42.	1234	щ	CFAH_MOUSE	9
20	38	42.	212	ш	OMPW_ECOLI	42
21	38	42.	230	щ	VIB8_AGRT9	agrobacter
22	38	42.	230	μ.	VIB8_AGRTU	-
23	38	42.	540	سر	Y968 TREPA	
24	38	42.	551	_	SYR_CHLTE	Q8kgf3 chlorobium
25	38	42.	607	H	HTPG_FUSNN	
26	38	42.	727	_	YK82_SCHPO	
27	38	42.	771	_	SM3A_HUMAN	
28	38	42.	772	_	SM3A_CHICK	7
29	38	42	772	_	SM3A_MOUSE	
30	38	42.2	772	_	SM3A_RAT	
31	38	42.	876	_	SYA_STAEP	7
32	37.5	41.	387	۳	SUCC_MYCTU	P71559 mycobacteri
33	37.5	41.7	393	ш	SUCC_MYCLE	Q9z5h8 mycobacteri

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1 VSKLEASTIRQ-EYYFGDA 18

Query Match 88.3 Best Local Similarity 94.7 Matches 18; Conservative

88.3%; Score 79.5; DB 1; Length 383; 94.7%; Pred. No. 1.8e-06; tive 0; Mismatches 0; Indels

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Q8y493 listeria mo	Q927t2 Listeria in	Q9x5m0 mycobacteri	P98080 caenornabai	094415 schizosacch	P28049 xenopus tae	P34692 caenorhabdi		P22816 drosophila			

ALIGNMENTS

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EMBL; S80954; AAB35931.1; InterPro; IPR006234; Lupus_La_dom. InterPro; IPR006539; Lupus_La_dom. InterPro; IPR000563; RNA_rec_mot. Pfam; PF00075; rrm; 1. Pfam; PF00303; La; 1. PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00715; LA; 1. PROSITE; PS00102; RRM; 1. PROSITE; PS00102; RRM; 1. PROSITE; PS00102; RRM; 1. PROSITE; PS00103; RRM RNP 1; FALSE NEG. RNA-binding; Nuclear protein; DNA-binding. RNA-BINDING (RRM). DOMAIN 141 228 RNA-BINDING (RRM). DOMAIN 141 228 RNA-BINDING (RRM).	NCBI TaxID=7160; [1]TaxID=7160; [2]TaxID=7160; [3]TaxID=7160; [3]TaxID=7160; [4]TaxID=7160; [5]TaxID=7160; [5]TaxID=7160; [6]TaxID=7160; [7]TaxID=7160; [8]TaxID=7160; [9]TaxID=7160; [9]TaxID=7	AEDAL JUL-199 JUL-199 JUL-199 protein les alboj

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A; Molecule type: DNA
A; Residues: 1-1036 <KLE>
A; Cross-references: GB: AB000783; TIGR: BB0140
A; Experimental source: strain B31
C; Superfamily: cation efflux system membrane protein czcA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acriflavine resistance protein (acrB) homolog - Lyme disease spirochete C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000 C;Accession: D70117
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A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete,

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70117
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A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein AF2348 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec.1997 #sequence_revision 05-Dec.1997 #text_change 22-Oct-1999 C;Accession: D69543
                                                                                                                                                                                                           A;Cross-references: GB:AE001114; GB:AE000782; NID:g2689437; PIDN:AAB91315.1; PID:g26507
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsor.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Residues: 1-112 <KLE>
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                                                 2 SKLEASTIRQEYYFGDA 18
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Search completed: September 10, 2004, 18:02:39 Job time: 16.0782 secs

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A;Accessum ....
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-642 <STO>
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04471.1; GSPDB:GN00
A;Cross-references: GB:AP001509; GB:BA0000004; NID:g10173176; PIDN:BAB04471.1; GSPDB:GN00
                                                                                                                                        RESULT 11
C96636
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir: Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC transporter (permease) BH0752 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans (c;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: H83743
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R;Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding protein PD2 - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
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                                                       hypothetical protein T7P1.19 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96636
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A; Residues: 1-632 <SAT>
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A; Accession: T06586
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A; Description: Identification of a novel family of DNA-binding
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8; Conserv
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Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
            A;Accession: A;Accession: A;Accession: A;Accession: A;Accession: Type: DNA
A;Rosidues: 1-633 <QUE>
A;Cross-references: EMBL;AL049659; GSPDB:GN00061; ATSP:T29H11.90
A;Cross-references: cultivar Columbia; BAC clone T29H11
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87591
                                                                                                                                                                                                                                                                                                              C;Accession: T06703
R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, submitted to the Protein Sequence Database, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T29H11.90 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #t. C;Date: 23-Apr-1999 #t
A; Gene: ATSP: T29H11.90
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A; Accession: T06703
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C;Superfamily: cycH protein
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A;Molecule type: DNA
A;Residues: 1-370 <STO>
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A; Residues: 1-322 < STO>
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cystathionine beta-synthase (EC 4.2.1.22) - yeast N;Alternate names: protein G6667; protein YGR155w C;Species: Saccharomyces cerevisiae C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 C;Accession: A48661; S48505; S42686; S60445; B5576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C/Superfamily: ribonucleoprotein La; ribonucleoprotein C/Keywords: phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology <RF F;113-118/Region: RNA-binding RNP2 motif F;151-158/Region: RNA-binding RNP1 motif
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                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-507 <CHE>
A;Residues: 1-507 <CHE>
A;Cross-references: GB:X72922; NID:g296134; PIDN:CAA51426.1; PID:g296135
A;Description: Identification of the structural gene of cystathionine bet
                                                                                                                                                                                                                                                                                                                                          R;Cherest, H.; Thomas, D.; Surdin-Kerjan, Y.
J. Bacteriol. 175, 5366-5374, 1993
A;Title: Cysteine biosynthesis in Saccharomyces cerevisiae
A;Reference number: A48661, MUID:93374830; PMID:8366024
A;Accession: A48661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Semsei, I.; Troester, H.; Bartsch, H.; Schwemmle, M.; Igloi, G.L.; Bachmann, M. Gene 126, 265-268, 1993
A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection A;Reference number: JC1494; MUID:93246255; PMID:7916708
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C;Date: 24-Feb-1994 #sequence_revision 26
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A;Cross-references: EMBL:D16502; NII R;Ono, B.I.; Kijima, K.; Inoue, T.; Yeast 10, 333-339, 1994
                                                                            A;Molecule type: DNA
A;Residues: 1-292,'T',294-507 <ONO>
                                                                                                                                                         A; Reference number: S48505
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A;Experimental source: liver
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A; Residues: 1-415 <SEM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text_change 21-Jul-2000;Accession: A48661; S48505; S42686; S60445; B55760; S64464; S33202;Cherest, H.; Thomas, D.; Surdin-Kerjan, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Comment: This protein associates with a variety of small RNA molecules,
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                           NID:g391939; PIDN:BAA03952.1; PID:g416161
T.; Miyoshi, S.I.; Matsuda, A.; Shinoda, S.
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Pred. No. 7.
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Pred. No. 7
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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-451 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75620.1;
A; Cross-reference: Strain PCC 7120
                                                                                                                                                                                                                                                                                                              UDP-N-acetylglucosamine pyrophosphorylase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AB2296
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A;Residues: 1-507 <VAN>
A;Cross-references: EMBL:Z72940; NID:g1323262; PIDN:CAA97169.1; PID:g1323263; MIPS:YGR1
A:Experimental source: strain S288C
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Proc. Natl. Acad. Sci. U.S.A. 91, 6614-6618, 1994
A;Title: A yeast system for expression of human cystathionine beta-synthase: structural
A;Reference number: A55760; MUID:94294429; PMID:8022826
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A. Title: The sequence of a
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A;Residues: 2-11 <ON2>
R;Skala, J.; Nawrocki, A.;
Yeast 11, 1421-1427, 1995
A; Gene: alr3921
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: cystathionine beta-synthase; CBS homology C;Keywords: carbon-oxygen lyase; cysteine biosynthesis; homotetram F;2-507/Product: cystathionine beta-synthase #status experimental F;376-424/Domain: CBS homology <CBS>
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A; Cross-references: SG
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A; Accession: S64464
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A; Residues: 1-61,63-128,'Y',130-406,'Y',408-435,'VE',438-440,'V',442-480,'E'
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A;Reference number: $42686; MUID:94287710; PMID:8017103
                                                                                                                                                                              A; Reference number: AB1807; A; Acçession: AB2296
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DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic
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                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                R; Kaneko, T.; Nakamura,
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                                                                                                                                                                                                                                                                      , Y.; Wolk, C.P.; Kuritz,
S.; Sugimoto, M.; Takazaw
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                                                                                                                                                                                                        Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                               Takazawa,
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                                                                                                                                                                                                                                                                               Sasamoto, S.;
M.; Yamada, M.
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N-acetylglucosamine-1-phosphate uridyltransferase

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ay act as a transcription termination factor.

C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
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A;Title: Ribonucleoprotein SS-B/La belongs to a protein A;Reference number: S03848; MUID:89202037; PMID:2468131
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ribonucleoprotein
                   A31888
                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: This protein associates with a variety of small RNA molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S03849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Chan, E.K.L.;
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A; Residues: 1-365 <BEV>
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A;Experimental source: cultivar Columbia; BAC clone F25G13
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Residues: 1-404 <CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Bos primigenius taurus (cattle)
;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                               228-404/Domain: phosphorylated #status predicted <PHY>
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Best Local :
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118/Region: RNA-binding RNP2 motif
158/Region: RNA-binding RNP1 motif
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                                                                                                                                1 VSKLEASTIRO-EYYFGD 17
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   human
                                                                                                                                                                                       48.3%;
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2; Mismatches
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Pred. No. 7.
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                 A; Introns:
C; Superfam:
                                                                                                              C;Genetics:
                 Superfamily: ribonucleoprotein
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A;Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; P:C;Comment: This protein associates with a variety of small RNA ayactas a transcription termination factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Characteristics and epitope mapping of a cloned A;Reference number: S11013; MUID:88199081; PMID:2452201 A;Accession: S11013
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C;Date: 21-May-1990 #sequence revision 26-May-1994 #text change 22-Jun-1999
C;Accession: A31888; S0348; Ā22956; A61051; S11013; I55553; I70205; I70206;
R;Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
                                                                     A; Map position: 2
                                                                                                A;Cross-references: GDB:125359; OMIM:109090
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A; Residues: 279-342 < RE3>
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A;Residues: 174-224 <RE2>
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A; Residues: 81-107 < RES>
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A; Residues: 'E',55-287,'V',289-408 <STU>
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A; Residues: 1-19, 'E', 21-47 < NYM>
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A;Title: Demonstration of an amino terminal La epitope reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 45-97,'LK' <CH3>
A;Cross-references: GB:J04205
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
A;Reference number: A22956; MUID:85166283; PMID:3856888
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A;Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1;
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A;Residues: 1-408 <CHA>
A;Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1;
R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
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22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2
ly: ribonucleoprotein La; ribonucleoprotein repeat homology
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phosphoprotein; RNA binding

OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11; Search time 14.0782 Seconds (without alignments) 122.988 Million cell updates/sec

Title: Perfect score: Sequence: US-09-836-073-18 90 1 VSKLEASTIRQEYYFGDA 18

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29		28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4	ω	N	ם	Result No.
						39		39.5	40	40	40	40	40	40	40	41	41	41	41	42	42	42	43	ω	43.5	43.5	44	52.5	52.5	Score
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Query Match

58.3%; Score 52.5;

DB 2; Length 390;

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T45501 T15874 C85706	AG1704 AH1333 NBMSH	G83718 A69787	H86508 H81556 AF2304	H49936 T07617 E72113	S12227
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ALIGNMENTS

A;Cross-relevences: GB:U32988; NLD:9488499; FLD:9488479 C;Genetics: A;Gene: FlyBase:La A;Gene: FlyBase:La A;Cross-references: FlyBase:FBgn0011638 C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: RNA binding	revision 19-Ja phila melanog [D:94309661; F	AIIRQVEYYFGDA 65 a - fruit fly (Drosophila melanogaster) la melanogaster	Base:La erences: FlyBase:FBgn ly: ribonucleoprotein leucine zipper; RNA i leucine f 58.3%; ch 58.7%; 1 Similarity 66.7%; 12; Conservative	R;Bai, C.; Li, Z.; Tolias, P.P. Mol. Cell. Biol. 14, 5123-5129, 1994 A;Title: Developmental characterization of a Drosophila RNA-binding protein homologous { A;Reference number: A53773; MUID:94309632; PMID:8035794 A;Raccession: A53773 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-390 <bai> A;Cross-references: GB:U07652; NID:g464019; PIDN:AAA20518.1; PID:g464020 C;Genetics:</bai>	RESULT 1 A53773 La/SS-B homolog D-la - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000 C;Accession: A53773

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RESULT 13
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILIGATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 46290
                                    GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46290, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                          Sequence 69520, Application US/10425114
Publication No. US20040034888A1
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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   APPLICANT:
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APPLICANT: Kovalic David K
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TYPE: PRT
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ORGANISM: Glycine max
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Kovalic, David K. Screen, Steven E
                                  Zhou, Yihua
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Pred. No.
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Pred. No.
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US-09-836-073-19
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                                                                            GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054825
FILE REFERENCE: 220002054826

FILE REFERENCE: 20002054826

FILE
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CURRENT FILING NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 106767
                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09836073 Patent No. US20020173475A1
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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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Pred. No. 10;
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Pred. No.

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RESULT 7
US-10-437-963-179489
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US-10-437-963-179489
                                                          ; OTHER INFORMATION: Clone US-10-437-963-134637
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Best Local S
Matches 7
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Matches 9; Conservative
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                                                                                                                                                                       SEQ ID NO 134637
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Query Match
Best Local Similarity
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                                                                                                                                                                                      APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
FULL REFERENCE: 38-21(53221)B
FULL REFERENCE: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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                                                                                                                                                     LENGTH: 405
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Barbazuk, Brad
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38.9%;
                                                                          ID: PAT_MRT4530_36391C.1.pep
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Pred. No. 2
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 Score 53; DB 16; Length 405; Pred. No. 3.7;
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SEQ ID NO 254661
LENGTH: 143
                                                                    Best Loc
Matches
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SEQ ID NO 66921
LENGTH: 357
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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Matches 9; Conserv
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                                                                                                  Query Match
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-231(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                          APPLICANT: Tabaská, Jack E
APPLICANT: COZO, YONGWei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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ORGANISM: Glycine max
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                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                      OTHER INFORMATION: Clone ID: UC-ZMFLB73148E12_FLI.pep
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                                                                                     Local Similarity
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163 DDPVPKIRKQVEYYFSDI 180
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                                1 DDADQRIIKQLEYYFGNI 18
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Kovalic, David K.
Screen, Steven E
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                                                                    Conservative
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                                                                                    53.7%;
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52.9%; Pred. No. 2
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                                                                                     Score 51; DB Pred. No. 6.8;
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US-10-177-478-8
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US-10-424-599-258874
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Sequence 8, Application US/10177478
Publication No. US20030165903A1
GENERAL INFORMATION:
APPLICANT: Dang, Van-Jinh
APPLICANT: Okamuro, Jack
TITLE OF INVENTION: Chimeric Histone Acetyltransferase
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 11696-037001
CURRENT APPLICATION NUMBER: US/10/177,478
CURRENT FILING DATE: 2002-06-21
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LENGTH: 467
TYPE: PRT
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SEQ ID NO 258877
LENGTH: 174
TYPE: PRT
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APPLICANT:
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TITLE OF INVENTION: Sy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
RUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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NAME/KEY: unsure
LOCATION: (1)..(467)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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les 9; Conserv
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50.0%;
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Pred. No. 0.48;
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Pred. No. 0.17;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 467;
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; SEQ ID NO 8
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana US-10-177-478-8
                               ; FEATURE:
; OTHER INFORMATION: Clone ID:
US-10-767-701-45524
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                                                                                                                                                                                                                                                                                                                                                                                            US-10-767-701-45524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Xenopus US-09-836-073-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 15
LENGTH: 18
TYPE: PRT
                                                                                                        APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(3535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45524
LENGTH: 376
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 45524, Application US/10767701 Publication No. US20040172684A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020173475A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/09836073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: U.S. PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                     ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 57.9%;
Local Similarity 56.2%;
nes 9; Conservative
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DLDTKICEQIEYYFGD 17
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 56.8%;
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                                                    SORBI-28MAY03-C33606_1.pep
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Pred. No. 0.067;
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Pred. No. 0.87;
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Score
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 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18
Length 376;
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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
Published Applications AA:*

1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2-6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

8: /cgn2-6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

10: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2-6/ptodata/1/pubpaa/US10E_PUB.pep:*

18: /cgn2-6/ptodata/1/pubpaa/US10E_PUB.pep:*
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95
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143.151 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1335176 seqs, 320689617 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1335176
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	95	100.0	18	ا و	US-09-836-073-17	Sequence 17, Appl
2	59	62.1	174	12	US-10-424-599-258877	Sequence 258877,
ω	59	62.1	467	12	US-10-424-599-258874	Sequence 258874,
4	57	60.0	411	14	US-10-177-478-8	Sequence 8, Appli
51	5 5	57.9	18	9	US-09-836-073-15	Sequence 15, Appl
σ	54	56.8	376	16	US-10-767-701-45524	Sequence 45524, A
. 7	54	56.8	453	16	US-10-437-963-179489	Sequence 179489,
œ	53		405	16	US-10-437-963-134637	Sequence 134637,
9	51	53.7	143	12	US-10-424-599-254661	Sequence 254661,
10	51	53.7	357	12	US-10-425-114-66921	Sequence 66921, A
11	51	53.7	395	12	US-10-424-599-254664	Sequence 254664,
12	51	53.7	489	16	US-10-767-701-46290	Sequence 46290, A
13	51	53.7	490	12	US-10-425-114-69520	Sequence 69520, A
14	51	53.7	511	16	US-10-437-963-106767	Sequence 106767,
15	50	52.6	16	9	US-09-836-073-19	Sequence 19, Appl

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
45	45	45	45	46	46	46	46	46	46	46	46	47	47	47	47	48	48	48	48	48	48	48	48	48	48	48	49	49	49
47.4	47.4	47.4	47.4	48.4	48.4	48.4	48.4	48.4	48.4	48.4			49.5	49.5	49.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	51.6	51.6	51.6
1076	223	198	18	161	9	39	39	39	39	39	39	343	199	108	108	936	420	397	385	385	245	112	112	112	112	112	488	401	303
14	13	12	9	16	14 4	14	14	12	10	9	9	16	16	15	14	14	16	9	16	14	16	16	16	16	16	16	12	12	12
US-10-116-949-6	-168-	US-10-296-115-1147	US-09-836-073-2	-963	US-10-054-611-26	US-10-054-295-26	US-10-053-758-26	US-10-325-810-216	US-09-438-486-26	US-09-766-253-26	US-09-843-676-26	US-10-437-963-111769	-10-767-701-5937	US-10-395-032-41	US-10-006-869-41	US-10-174-677-52	US-10-437-963-128072	US-09-738-626-5064	US-10-624-080-1	US-10-242-943-16	US-10-624-080-5	-10-624-08	US-10-624-080-11	US-10-624-080-10	US-10-624-080-9	US-10-624-080-3	US-10-424-599-272690	10-42	US-10-425-114-45759
Sequence 6, Appli		Sequence 1147, Ap						216		Sequence 26, Appl			Sequence 59379, A	Sequence 41, Appl	Sequence 41, Appl	Sequence 52, Appl	Sequence 128072,	ū	Sequence 1, Appli	16, App	5, Appl			Sequence 10, Appl	9	•	e 27	Sequence 254663,	æ

ALIGNMENTS

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US-10-424-599-258877; Sequence 258877, Application US/10424599; Publication No. US20040031072A1
                                                                RESULT 2
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                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: C. elegans US-09-836-073-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-836-073-17
                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/09836073 Patent No. US20020173475A1
                                                                                                                                                                                                                  Query Match 100.0%; Score 95; DB 9; Best Local Similarity 100.0%; Pred. No. 2.7e-08; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                 1 DDADQRIIKQLEYYFGNI 18
                                                                                                                                                          1 DDADQRIIKQLEYYFGNI 18
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JOSEPH JAMEN JAMEN
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US-09-430-323-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
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Best Local Similarity 63.
Matches 7; Conservative
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 09-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cech, Thomas R.
                                     NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsen
                                                                                                                                                     Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIKQLEYYFGN 17
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                        Chapman, Karen в
Morin, Gregg В.
Harley, Calvin
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Nakamura, Toru
Chapman, Karen B.
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09-MAY-1997
V: 53-
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US-09-430-323-26
                                                                                         Query Match 48.4%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRILING DATE: 05/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION CUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION DATA: APPLICATION DATA: 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-196
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                             STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                            7 IIKQLEYYFGN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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STATE: California
COUNTRY: United States of America
ilroveyyfgd 11
                                                                                                                                                                                                                                                                                                            LENGTH: 39 amino acids
TYPE: amino acid
                                                                                                                  Score 46; DB 4; Length 39; Pred. No. 0.63;
                                                                                              Mismatches
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Search completed: September 10, 2004, 18:05:11 Job time : 16.8883 secs

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APPLICATION NUMBER: US/08/974,549A

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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
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LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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APPLICATION NUMBER: US 08/844,419
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
CURRENT APPLICATION DATA:
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APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,429
REFERENCE DOCKET NUMBER: 015389-002930US
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CLASSIFICATION:
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CITY: San Francisco
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                                                                                                                      COUNTRY:
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Nakamura, Toru
Chapman, Karen B.
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Pred. No. 0.63;
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US-08-854-050-26
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Patent No. 6261836
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Best Local S
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APPLICANT: Cech, Thomas
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INFORMATION FOR SEQ ID NO:
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NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
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FILING DATE: 06-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
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APPLICATION NUMBER:
      APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                              APPLICANT:
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LENGTH: 39 amino acids
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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FILING DATE: 14-AUG-1997
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CLASSIFICATION:
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FILING DATE: 01-OCT-1996
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|ILRQVEYYFGD 11
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                                                                                                              Nakamura,
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                                                US-09-535-852-41
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SEQ ID NO 41
LENGTH: 108
TYPE: PRT
ORGANISM: Mus musculus
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US-09-839-542B-41
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-859-41
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                                                                 RESULT 10
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Sequence 41, Application US/09535852 Patent No. 6638911 GENERAL INFORMATION:
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APPLICANT: GOUY, BAYBARA J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Applicat Patent No. 6358920 GENERAL INFORMATION:
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Matches
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity 47.1%;
Matches 8; Conservative
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APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2001-04-20
CURRENT FILING DATE: 2001-04-20
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Conservative
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Pred. No. 1.4;
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Pred. No. 1
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                                                                                                                                                                                                                Length 108
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US-08-851-843A-26
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US-09-540-236-2229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2229, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2229
LENGTH: 191
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CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08851843A Patent No. 6093809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blachuk, Orest W. APPLICANT: Symonds, James N. APPLICANT: Gour, Barbara J.
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                             APPLICANT:
                                                                                                 APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 108
                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                 APPLICANT:
                                 STREET: Two Embarcac
CITY: San Francisco
STATE: California
              COUNTRY:
                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 49.5%;
Local Similarity 47.1%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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8; Conservat
94111
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                               California
              United States of America
                                                                                                                                                                                                           Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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Pred. No. 2.
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Pred. No. 1.
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TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400

REFERENCE/DOCKET NUMBER:

44301-Z/JPW/AGL

TELEPHONE: 121

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; MOLECULE TYPE: protein US-08-516-801-2
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                                                                                                                                US-08-248-355-2
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/248,355 FILING DATE: 24-May-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                          TELEPHONE: (212) 977-9550
TELEPAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 441
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goff, Stephen P.
APPLICANT: Kalpana, Ganjam V.
TITLE OF INVENTION: A cDNA Clone of the Human Ini-1 Gene Encoding TITLE OF INVENTION: a Protein That Binds to the HIV-1 Integrase; TITLE OF INVENTION: and Its Use in Antiviral Therapy NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 30 Rock
                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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 DOSDORVIIKLNIHVGNI 273
                                DDADQRIIKQLEYYFGNI 18
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30 Rockefeller Plaza
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                                                                                50.5%;
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Pred. No.
                                                                4; Mismatches
                                                                                Score 48; DB Pred. No. 3.9;
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RESULT 6

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US-09-167-206-16
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PCT-US95-06683-2
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LENGTH: 385
TYPE: PRT
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APPLICANT: Nandabalan, Krishnan
APPLICANT: Schulz, Vincent P.
APPLICANT: Yang, Meija
APPLICANT: Yang, Meija
APPLICANTION: NIK1 PROTEIN AND NIK1 PROTEIN COMPLEXES
FILE REFERENCE: 1996-521 NIK1 PROTEIN COMPLEXES
CURRENT APPLICATION INMBER: US/09/167,206A
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9506683
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Kalpana, Ganjam V.
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Patent No. 6476193
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                                                                          TELEFAX: (212) 391-052
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,355
FILING DATE: 24-May-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
                                                                                                        JIECUM: 1210
TELEPHONE: 1212)
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 24-May CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                      TOPOLOGY:
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256 DQSDQRVIIKLNIHVGNI 273
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9; Conservative
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                                  1: 385 amino acids amino acid
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Y: U.S.A.
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                                                                                                                                    (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cooper & Dunham LLP
protein
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                                                                                                                  391-0525
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A cDNA Clone of the Human Ini-1 Gene Encoding
a Protein That Binds to the HIV-1 Integrase;
and Its Use in Antiviral Therapy
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Pred. No.
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PCT-US95-06683-3
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                                                                             Sequence 3, Application PC/TUS9506683
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Kalpana, Ganjam V.
TITLE OF INVENTION: A CDNA Clone of the Human Ini-1 Gene Encoding TITLE OF INVENTION: A Protein That Binds to the HIV-1 Integrase;
TITLE OF INVENTION: and Its Use in Antiviral Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08248355
Patent No. 6222024
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Kalpana, Ganjam V.
APPLICANT: Kalpana, Ganjam V.
TITLE OF INVENTION: A CDNA Clone of the Human Ini-1 Gene Encoding TITLE OF INVENTION: a Protein That Binds to the HIV-1 Integrase;
TITLE OF INVENTION: and Its Use in Antiviral Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/248,355
FILING DATE: 24 May-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44301
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
COUNTRY: U.S.A.
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STRANDEDNESS: sin
TOPOLOGY: linear
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ADDRESSEE:
STREET: 11
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Similarity 50.0%;
9; Conservative
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E: Cooper & Dunham LLP
1185 Avenue of the Americas
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Pred. No. 1
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Patent No. 5872213

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Kalpana, Ganjam V.
TITLE OF INVENTION: A cDNA Clone of the Human Ini-1 Gene Encoding a
TITLE OF INVENTION: Protein That Binds to the HIV-1 Integrase; and Its Use in Anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06683
FILING DATE: 24-May-1995
CLASSIFICATION:
APPLICATION DATA:
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CLASSIFICATION DATA:
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APPLI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/516,801
FILING DATE: 18-August-1995
CLASSIFICATION: 530
CLASSIFICATION: 530
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TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STRANDENESS: sing
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: N
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NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: John P. White, Esq.
REGISTRATION NUMBER: 28,678
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FRAGMENT TYPE: N-terminal
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Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Cooper & Dunham LLP
1185 Avenue of the Americas
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Pred. No. 1.9;
4; Mismatches
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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                                                                                                           GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES
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(without alignments)
58.488 Million cell updates/sec
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RESULT 1 US-08-516-801-3

ALIGNMENTS

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	ტ	Ŋ	4	ω	N	ш	Result No.
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US-09-430-323-25	-08-854-050-2	-974-5	US-08-851-843A-25	US-09-316-630-4	US-09-316-630-3	US-09-543-681A-5508	US-09-470-443-4	-443	US-09-470-443-6	US-09-721-456-216	- 1	US-09-430-323-26	US-08-854-050-26	US-08-974-549A-216	US-08-851-843A-26	US-09-540-236-2229	US-09-535-852-41	US-09-839-542B-41	-4	PCT-US95-06683-2	US-09-167-206-16	US-08-248-355-2	US-08-516-801-2	PCT-US95-06683-3	US-08-248-355-3	US-08-516-801-3	ID
Sequence 25, Appl	e 25, 1	e 215,	e 25, 1	e 4, 1	e 3,	e 55	, Apr	e 2,	e 6,	e 216	e 216	e	e 26,	Sequence 216, App	e 26, 1	e 2229	•	e 41,	41,	2,	e 16,	e 2,	2	Sequence 3, Appli	-	Sequence 3, Appli	Description

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43 45.3 38 4 US-09-721-456-215 43 45.3 498 4 US-09-107-532A-6991 41 43.2 21 4 US-09-107-532A-6991 41 43.2 108 4 US-09-187-859-43 41 43.2 108 4 US-09-187-859-43 41 43.2 108 4 US-09-839-542B-43 41 43.2 108 4 US-09-839-542B-43 41 43.2 265 4 US-09-328-352-4347 41 43.2 265 4 US-09-389-039A-9106 41 43.2 775 3 US-09-489-039A-9106 41 43.2 775 3 US-09-188-404-4 40 42.1 185 3 US-09-281-259-2 40 42.1 185 3 US-09-149-476-394 40 42.1 185 3 US-09-94-295-1 40 42.1 335 4 US-09-540-236-2303 41.1 72 4 US-09-107-532A-3822	ئار 1ن	64	43	42	41	40	39	38	. 37	36	35	34	33	32	31	30	29	20
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4 US-09-721-456-215 4 US-09-175-552A-6991 4 US-08-475-952-00 4 US-09-187-859-43 4 US-09-187-852-43 4 US-09-328-352-4347 4 US-09-328-352-4347 4 US-09-489-039A-9106 2 US-09-188-40-4 3 US-09-188-40-4 3 US-09-188-40-4 4 US-09-281-259-4 4 US-09-281-259-4 4 US-09-281-259-4 5 US-09-281-259-4 6 US-09-149-476-394 6 US-09-140-476-394 7 US-09-140-476-394	72	335	186	185	108	775	775	775	775	626	265	108	108	108	21	498	38	Ĺ
US-09-171-456-215 US-09-107-522A-6991 US-08-475-955-20 US-09-187-859-43 US-09-839-542B-43 US-09-839-542B-43 US-09-281-352-4347 US-09-489-039A-9106 US-08-66-388-4 US-09-188-403-4 US-09-188-4 US-09-18	4	4	4	w	4	w	ω	ω	N	4	4	4	4	4	4	4	4	ì
	US-09-107-532A-3822	US-09-540-236-2030	US-09-149-476-394	US-08-984-295-1	US-09-149-476-552	US-09-281-259-4	US-09-188-404-4	US-09-188-403-4	US-08-966-388-4	US-09-489-039A-9106	US-09-328-352-4347	US-09-535-852-43	US-09-839-542B-43	US-09-187-859-43	US-08-475-955-20	US-09-107-532A-6991	US-09-721-456-215	20 20 100
	3822, Ap	2030, Ap	394, App	1, Appli	552, App	4, Appli	4, Appli	4, Appli	4, Appli	9106, Ap	4347, Ap	43, App1	-	43, App1	20, App1	6991, Ap	215, App	

US-08-516-801-3 Sequence 3, Application US/08516801 Patent No. 5872213 Best Local Similarity 50.0%; Pred. No. 1.9; Matches 9; Conservative 4. Winner. GENERAL INFORMATION: APPLICANT: Goff, Stephen P. APPLICANT: Kalpana, Ganjam V. TITLE OF INVENTION: A cDNA Clone of the Human Ini-1 Gene Encoding a TITLE OF INVENTION: Protein That Binds to the HIV-1 Integrase; and Its Use in Anti COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/516,801 FILLING DATE: 18-August-1995 CLASSIFICATION: 530 ATTORNARY/AGENT INFORMATION: NAME: Take Position Pos TELEFAX: (212) 391-0526 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 204 amino acids TOPOLOGY: linea. MOLECULE TYPE: DN HYPOTHETICAL: N ANTI-SENSE: N FRAGMENT TYPE: N-terminal NAME: John P. White, Esq. REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 44: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TYPE: amino acid STRANDEDNESS: sir TOPOLOGY: linear STATE: New York COUNTRY: U.S.A. ZIP: 10036 STREET: 1185 A ADDRESSEE: E: Cooper & Dunham LLP 1185 Avenue of the Americas DNA (genomic) single 44301-Z/JPW/AGL Length 204; Indels 0 Gaps 0

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RESULT 13
Q69711
ID Q6971
AC Q6971
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DT 01-NO
DT 01-JU
DE Envell
GN ENV.
OS Human
OC Virus
ON NCELL
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RY MEDLI
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01-NOV-1996
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01-JUN-2003
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Q7ZQS0;
01-JUN-2003
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Pfam; PF00516; GP120; 1.
AIDS; Coat profet
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Lukashov V.V., Kuiken C.L., Boer K., Goudsmit J.;
"HIV type 1 subtypes in The Netherlands circulating
originating from AIDS-endemic regions.";
AIDS Res. Hum. Retroviruses 12:951-953(1996).
EMBL; L76905; AAC37965.1; -.
EMBL; L76905; AAC37965.1; capsid; IEA.
GO; GO:0019038; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
Sequence after Vertical Transmissi with HIV-1 Subtype A.";
J. Virol. 77:3050-3057(2003).
EMBL; AY175045; AA020524.1; -.
GO; GC:0019031; C:viral envelope;
InterPro; IPR000777; GP120.
                                                                                                         SEQUENCE FROM N.A.
STRAIN-mother IP6;
MEDLINE=2472311; PubMed=12584330;
Verhofstede C., Demecheleer E., De Cabooter N., Gamwanyumba F., Claeys P., Chohan V., Mandaliya K.,
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01-JUN-2003 (TrEMBLrel. 24, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Envelope glycoprotein (Fragment).
                                                                                                                                                                                            Human immunodeficiency virus 1. Viruses; Retroid viruses; Retro NCBI_TaxID=11676;
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NCBI_TaxID=11676;
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Search completed: Job time: 43.229

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MEDLINE=22472311; PubMed=12584330;
Verhofstede C., Demecheleer E., De Cabooter N., Ga
Mwanyumba F., Claeys P., Chohan V., Mandaliya K.,
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J. Virol. 77:3050-3057(2003).
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Similarity 61.5%;
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QEVVKQLRTYFGN
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342 AA;
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238
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                                      Score 48; DB Pred. No. 16; 2; Mismatches
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Pred. No. 16;
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Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (AUG-2001) ---:
                                                                                                                                                                                                                                                                                                                                                Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Ronning (Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., Vanaken (Peldblyum T.V., V.C., Wortman J.R., White O., Fraser C.M.; "Arabidopsis thaliana chromosome 5 BAC F13M11 genomic sequence."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY052365; AAK96556.1; -
EMBL; AY139801; AAM98107.1; -
EMBL; AY139801; AAM98107.1; -
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
AT5921160/T10F18_190 (Proline-rich protein family).
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GG; GO:0006413; P:translational initiatic
InterPro; IPR006630; Lupus La dom.
InterPro; IPR002955; P rich extensn.
InterPro; IPR001950; TIF_SUII.
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Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H
Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
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SEQUENCE 826 AA; 91377 MW;
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                                                                 DLRDRVLKQVEYYFSD 292
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Q9IWT4;
01-OCT-2000
01-OCT-2000
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01-NOV-1996
01-JUN-2003
                                                                                                                                                                     Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N., Colebunders R.C., St Louis M., Quinn T.C., Folks T.M., Lal "predominance of HIV type I subtype G among commercial sex from Kinshasa, Democratic Republic of Congo.";
AIDS Res. Hum. Retroviruses 17:361-365(2001).
EMBL; AF260442; AAF71590.1; -...
30; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR000777; GF120.
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SEQUENCE
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EMBL: Z47894; CAA87908.1; -...
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                                                                                                                                    Pfam;
AIDS;
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AIDS; Coat protein; Glycopr
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Scherpbier H.J., de Perre P., Boer K., Gc
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GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AΑ;
                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment)
                                                                   170
19351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10561 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.6%;
  51.6%;
52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01,
24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Last annotation update)
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Last annotation update)
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  Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; I
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4941876B98E6FFA8 CRC64;
                                                                     177B41DAF6F7FB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goudsmit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dekker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 93;
                       Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 7

OBOHIS

OBOHIS

OC OBOH
RESULT 8
Q7ZBB0
Q7ZBB0
Q7ZB
AC
Q7ZE
AC
Q7ZE
DT
01-J
DT
01-G
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Enve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMBL/GenB
EMBL; AF467897; AAL76269.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR002344; Lupus La.
InterPro; IPR000504; RNA_rec_mot.
pfam; pF05383; La; 1.
pfam; pF05383; La; 1.
pfam; pF00376; rrm; 1.
pfam; pF00376; rrm; 1.
SMART; SM00360; RRM; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus_La_dom.
InterPro; IPR006630; Lupus_La_dom.
Pfam; PF05383; La; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SEQUENCE 389 AA; 42100 MW; 10C186
Q7ZBB0
Q7ZBB0;
Q1-JUN-2003
01-JUN-2003
01-QCT-2003
Envelope gly
ENV:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obr.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Calliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2001) to the EMBL; AP003375; BAB90138.1; Gramene; Q8SOT8; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Untranslated region binding-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone:OJ1414_E05.";
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                                                                                                                                                                                                                                                                                                   Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50102; RRM; 1.
PS00030; RRM RNP 1; 1.
206 AA; 23992 MW;
                        glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DELCDRIVKQVEYYFSD 101
                                                                                                                                                                                                                                                        ESKICQQIEYYFGN
                                                                                                                                                                                                                                                                                                   DORIIKOLEYYFGN 17
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                                      (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
42100 MW;
                                                                                                                                                                                                                                                                                                                                                                       54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.8%;
                          (Fragment).
                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            Score 52;
                                                                                                                                                                                                                                                                                                                                                                           Pred
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10C1863EAB6FA7B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             965B62F7DFFB90E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                           .
No.
                                                                                                                                      211
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                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                            Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT
Q8T8V5
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                                                                  Query Match
Best Local S
Matches 8
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Best Local S
Matches
                                                                                                                                                  PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1
SEQUENCE 390 AA; 44869 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8T8V5;
Q8T8V5;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY075257; AAL68124.1; -. FlyBase; FBgn0011638; La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kiwelu I.E., Renjifo B., Chaplin B., Sam N., Nkya Kapiga S., Essex M.; Sesex M.; Wapiga S., Essex M.; Sesex M.; Sesx M.; Sesex M.; Sesex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                    InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0008098; F:5S rRNA primary 1
GO; GO:0003723; F:RNA binding; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LA OR CG10922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=TZMOE47146;
MEDLINE=22483018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                  Similarity
8; Conserv
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DQRIIKQLEYYFGN 17 :: ||:|:|||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQVAKQLERYFGN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12596722;
ifo B., Chaplin B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23512 MW;
                                                                                    52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21,
21,
25,
                                                                                                                                                  1; 1.
                                                                  Score 50; DB
Pred. No. 8.5;
5; Mismatches
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Last annotation update)
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D94732D39FC1497B CRC64;
                                                                                                                                                      797FDE26B903C909 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                            transcript binding; IDA.
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                                                                                      DB 5;
8.5;
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1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases.
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                                                                                                          Length 390;
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                                                                Gaps
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RESULT
080567
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Best Local S
Matches 9
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( O80567; Q9C5X1;
( O80567; Q9C5X1;
( O1-NOV-1998 (TrEMBLrel. 08, Created)

O1-NOV-1998 (TrEMBLrel. 21, Last sequence update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Expressed protein (VirF-interacting protein FIP1) (Hypothetical Expressed protein) (Ar2943970/F6E13.10).

B protein) (Ar2943970/F6E13.10)

N AT2643970 OR F6E13.10/AT2643970.

N AT2643970 OR F6E13.10/AT2643970.

S Arabidopsis thaliana (Mouse-ear Cress).

S Permatophyta; Magnoliophyta; eudicotyledons; core eudicots; ros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La dom.
InterPro; IPR006630; Lupus_La dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00715; RAM; 2.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;
STRAIN=cv. Columbia;
Rounsley S.D., Kaul S., Lin X.,
Rounsley S.D., Kaul S., Lin X.,
Brandon R.C., Sykes S.M., Mason
Somerville C.R., Venter J.C.;
Submitted (JAN-1998) to the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv.
Town C.D.,
Submitted (
                                                                                                                                                                            Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema B., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Yamada K., Banh J., Onodera C.S., Quach
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Mayda E., Tzfira T., (
"Arabidopsis thaliana
Submitted (DEC-2000) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                           SEQUENCE FROM N.A.
Kim C.J., Chen H.,
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STRAIN=cv. Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                      gth cDNA of (SEP-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FEB-2002)
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                        Chen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Columbia;
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     Cheuk R., Carninci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48996 MW;
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56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Citovsky V.;
a VirF-interacting protein
to the EMBL/GenBank/DDBJ o
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                                                                                                                                    F6E13.10/At2g43970
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Last annotation update)
Eracting protein FIP1) (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases.
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Pred. No.
Koesema E., M
                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases.
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T.M., Kerlavage A.R., Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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     Meyers M.C.,
K., Goldsmith
                                                                                                                                    (GI:3212854).";
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                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                             databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIP1."
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udicots; rosids;
     Shinn
h A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          м.D.,
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RESULT DESCRIPTION OF THE PROPERTY OF THE PROP
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Best Local S
Matches 8
                                                                                                                  RNA-binding protein-like.

OJ1414_E05.3.
Oryza sativa (japonica cultivar-group).

Eukaryota, Viridiplantae; Streptophyta; Em
Spermatophyta; Magnollophyta; Lillopsida;
Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                            28SOT8
Q8SOT8;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Ngyen M.,
Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis CDNA clones.";
"Arabidopsis CDNA clones.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narus Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada Yu G., Shinozaki K.K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis cDNA clones."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005634; C:nuclous; IEA.
GO; GO:0003722; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein SEQUENCE 545 AA;
                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00302; LUPUSLA.
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nilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                            (TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                             Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
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Pred. No.
    moto K.;
genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E1A933261FE1ED80 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                389
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                                                                                                                                                                            Embryophyta; Tracheophyta; ; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Karlin-Neumann
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RESULT 3
Q94A38
ID Q94A
AC Q94A
DT 01-D
DT 01-D
DT 01-O
DT 01-O
DT AT59
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Q9FL36
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Best Local S
Matches
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Best Local S
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Pfam; PF00076; xrm; 1.

PRINTS; PR00302; LUPUSLA.

SMART; SM00715; LA; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS50030; RRM RNP 1; FALSE NEG.

SEQUENCE 396 AA; 43631 MW; AZDEZ8A4AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB010698; BAB11080.1; -.
GO; GC:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus_La
InterPro; IPR00630; Lupus_La dom.
InterPro; IPR006530; Lupus_La dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
Pfam; PF00076; rrm; 1.
SMART; SM00310; RRM; 1.
SMART; SM00310; RRM; 1.
SMART; SM00360; RRM; 1.
SMART; SM00360; RRM; 1.
094A38 PRELIMI
094A38;
01-DEC-2001 (TYEMBL
01-DEC-2001 (TYEMBL
01-OCT-2003 (TYEMBL
AT5946250/MPL12_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oi-MAR-2001 (TrEMBLrel. 16, Created)
ol-MAR-2001 (TrEMBLrel. 25, Last sequence update)
ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
similarity to RNA-binding protein.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. V. features of the regions of 1,381,565 bb covered by twenty one physically assigned P1 and TAC clones.";
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Columbia; MEDLINE=98344145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FL36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FL36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _TaxID=3702;
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10 DDADQKIIKQLEYYFGNI 27
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DELNQKIIRQVEYYFSD 106
                                                                                                                                                                                                                                                                                              DDADQRIIKQLEYYFGN 17
                              (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                           411 AA; 45655 MW;
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                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9679202;
                                                                                                                                                                                                                                                                                                                                                                  60.0%;
52.9%;
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25,
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                              Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                  Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92; DB 5;
Pred. No. 1.1e-06;
                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             A2EF62EB5B89B099 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411
                                                                                                                             422
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RESULT
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Best Local S
Matches
                                                                                                                                                                                                                               QTZTK2;
QTZTK2;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Q1-QCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to lupus LA protein homolog B.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carrinci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis CDNA clones."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Chan V.W., Ishida J., Jones T., Kamiya A., Kariin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H. Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC046654; AB446654.1; -.
GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7ZTK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
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GO; GO:0003723; F:RNA binding; IEA
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La dom.
InterPro; IPR006630; RNA_rec_mot.
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                                                                                                                     TISSUE=Embryo;
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                      NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Arabidopsis ORF clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.;
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9; Conserv
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                                                                                                                                                 FROM N.A.
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nilarity 52.9%;
Conservative
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Pred. No. 0.65;
6; Mismatches
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-836-073-17
95
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137.751 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                          SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                           sp_human:*
sp_invertebrate:*
sp_manmal:*
sp_mde::*
sp_mhc::*
sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_bacteriap:*
sp_bacteriap:*
                                   SUMMARIES
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Result No.	Score	Query Match	Length	DB	ij	Description
1	92	96.8	396	σį	001806	001806 caenorhabdi
N	57	60.0	411	10	Q9FL36	Q9fl36 arabidopsis
ω	57	60.0	422	10	Q94A38	Q94a38 arabidopsis
4	55	57.9	427	13	Q7ZTK2	Q7ztk2 xenopus lae
_υ	54	56.8	545	10	080567	O80567 arabidopsis
Φ	53	55.8	389	10	Q8SOT8	
7	52	54.7	206	13	Q8QHI5	Q8qhi5 gallus gall
80	50	52.6	211	15	Q7ZBB0	Q7zbb0 human immun
9	50	52.6	390	տ	Q8T8V5	Q8t8v5 drosophila
10	50	52.6	826	10	Q940X9	Q940x9 arabidopsis
11	49	51.6	93	15	Q77881	Q77881 human immun
12	49	51.6	170	15	Q9IWT4	Q9iwt4 human immun
13	48	50.5	90	15	Q69711	Q69711 human immun
14	48	50.5	341	15	Q7ZQS0	Q7zqs0 human immun
15	48	50.5	342	15	Q7ZQR9	Q7zgr9 human immun
16	48	50.5	342	15	Q7ZQP5	Q7zqp5 human immun

į	7	44	43	42	41	40	39	38	37	36	35	34	ü	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
į	4	46	46	46	46	46	46	46	46	46	47	47	47	47	47	47	47	47	47	48	48	48	48	48	48	48	48	48	48
		48.4	48.4	48.4	48.4		•	48.4	48.4	48.4	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	49.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5	50.5
	ر ا کر	351	351	351	351	342	128	102	102	102	934	898	401	343	143	115	115	114	102	890	863	859	397	394	385	385	376	342	342
;	7	15	15	15	15	15	15	15	15	15	11	11	13	10	15	15	15	15	15	4.	15	15	16	4	11	4	11	15	15
# · · · · · · · · · · · · · · · · · · ·	07Z0P9	Q7ZQQ0	Q7ZQQ1	Q7ZQQ2	Q7ZQQ3	Q7ZQR1	Q9QMB7	Q90AY3	Q90AN7	Q90AW6	Q91Y15	088193	Q7ZTI0	Q94LD0	Q9J6A7	Q74722	Q9YL52	Q9YL33	Q90AP7	Q8N4R3	Q8JBE4	011947	QBNQL9	Q9НВ36	Q9ESU1	Q9UBH2	Q9ESU0	Q7ZQP3	Q7ZQP4
	Q7zqp9 human immun	Q7zqq0 human immun	Q7zqql human immun	human	human	Q7zqrl human immun	/ human	human	human	human	mus mu		brac			human	human	human	7 human	ິ			coryne	-5	Brum 1	nomo	. mus	huma	human

ALIGNMENTS

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RESULT 15

DPOE MOUSE STANDARD; PRT; 2283 AA.

ID DPOE MOUSE STANDARD; PRT; 2283 AA.

AC Q9WF7; Q9QX50;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

T15-MAR-2004 (Rel. 43, Last annotation update)
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Best Local S
Matches 7
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Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                   EMBL;
EMBL;
EMBL;
                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase epsilon catalytic subunit.";
Biochim. Biophys. Acta 1445:363-371(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=99296371; PubMed=10366722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase epsilon, copolymerase II subunit A).
POLE OR POLE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50102; RRM; 1. 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; P
DOMAIN 111 187 RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X67859; CAA48043.1; -.
PIR; JC1494; JC1494.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR009504; RNA_rec_mot.
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang D., Knuuti R., Palosaari H., Pospiech H., Syvaoja J.E., "cDNA and structural organization of the gene Polel for the \mathfrak m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                           + {DNA} (N).

**CONSISTS OF TWO SUBUNITS (258 kDa and 55 kDa).

**SUBCELLULAR LOCATION: Nuclear.

**DOMAIN: The DNA polymerase activity domain resides in the N-terminal half of the protein, while the C-terminus is necessary for complexing subunits B and C. The C-terminus may also regulate the catalytic activities of the enzyme.

**SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                     replication.
CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N
                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION:
                 AF123502; //
AF126398; //
AF126377; //
AF126378; //
AF126379; //
AF126380; //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAKICHQIEYYFGD 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DORIIKOLEYYFGN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Participates in DNA repair and in chromosomal DNA
; AAD45244.1; -.
; AAD46482.1; -OINED.
; AAD46482.1; JOINED.
; AAD46482.1; JOINED.
); AAD46482.1; JOINED.
); AAD46482.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB Pred. No. 11; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Phosphorylation.
RNA-BINDING (RRM).
; 033FD9CC1E475F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 2.7.7.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 415;
                                                                                                                                                                                                                                                                                                                                                                            diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse
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                                                                                                                                                                          InterPro; IPR006172; DNA DOL B.
InterPro; IPR006134; DNA DOL B dom.
InterPro; IPR006133; DNA DOL B exo.
Pfam; PF00136; DNA DOL B; 1.
Pfam; PF00136; DNA DOL B exo; 1.
SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                          Transferase;
DNA-binding;
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                                                                                                                                                                                                                                                                            EMBL;
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AF126387;
AF126388;
AF126389;
AF126390;
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AF126383;
AF126384;
AF126385;
73
              2
                                 Similarity 6; Conserv
            DADORIIKOLEYYF
DEDKRLVSAVDYYF
                                                                    205
284
1309
1320
1386
1665
2086
2111
2283
                                  Conservative
                                                                                                                                                           Zinc-tinger;
                                                                                                                                                                    DNA-directed
                                                                                                                                                                                                                                                                          AAD46482.1;
AAD46482.1;
AAD46482.1;
AAD46482.1;
AAD46482.1;
AAD46482.1;
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AAD46482.
AAD46482.
AAD46482.
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                                                                                                                                                                                                                                                                  AAD46482.
                                                                           2235
205
284
1309
1320
1388
1665
2086
                                                                                                                                                                                                                                Pole
                                          46.3%;
42.9%;
                                                                    262025
98
               15
                                                                                                                                                          DNA polymerase;
Nuclear protein.
                                                                  Nuclear protein.

POTENTIAL.

D -> E (IN REF. 1; AAD45244).

T -> K (IN REF. 1; AAD45244).

G -> E (IN REF. 1; AAD45244).

K -> R (IN REF. 1; AAD45244).

K -> GJFL (IN REF. 1; AAD45244).

ALP -> GJFL (IN REF. 1; AAD45244).

T -> V (IN REF. 1; AAD45244).

I -> Q (IN REF. 1; AAD45244).

L -> Q (IN REF. 1; AAD45244).

L -> Q (IN REF. 1; AAD45244).
                                                                                                                                                                                                                                       JOINED
                                          Score 44; DB
Pred. No. 65;
                                   Mismatches
                                                                                                                                                                    DNA replication; DNA repair;
                                                  1;
                                   ω
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                                                 Length 2283;
                                   Indels
                                                                                                      1; AAD45244).
                                   0
                                   Gaps
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Search completed: September 10, 2004, 17:53:10 Job time: 8.24022 secs

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RESULT 13
ITA MOUSES
IID LIA MO
AC P3206
AC P320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Allschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

All Collins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

All Collins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

All Collins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

All Collins R.F., Jordan R., Farmer A.A., Rubin G.M., Hong L.,

All Collins R.F., Loquellano N.B., Bonaldo M.F., Caraninci P., Prange C.,

All Robard S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

All Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

All Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hilalan D.K., Touchman J.W., Green E.D., Dickson M.C.,

RA Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Botterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Thuman and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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P32067;
01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-11 FROM N.A.

Groelz D., Bachmann M.;

Submitted (OCT-1956) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: La protein plays a role in the transcription of RNA
-polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor forms
of RNA polymerase III transcripts including tRNA and 4.55, 55, 75,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Topfer F., Gordon T., McCluskey J.;
Topfer F., Gordon T., McCluskey J.;
"Characterization of the mouse autoantigen La (8S-B). Identificat
of conserved RNA-binding motifs, a putative ATP binding site and
reactivity of recombinant protein with poly(U) and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93203630; PubMed=8454877;
MEDLINE=93203630, PubMed=8454877;
MCCluskey J;
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVB/N; TISSUE=Mammary gland; MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homolog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                       SUBUNIT: Interacts with DDX15 (By similarity). SUBCELLULAR LOCATION: Nuclear (Probable). PTM: Phosphorylated (By similarity)
                                                                                                                                                            PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
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                                                                                                                                                                                                                                                                                           7-2 RNAs.
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(Rel. 27, Last sequence update)
(Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150:3091-3100(1993).
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Rodentia;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ں</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification
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Best Local
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Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                              LA RAT
P38656;
01-FEB-1995
01-FEB-1995
28-FEB-2003
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                                                                                       This
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PROSITE; PS00030; RRM RNP 1; 1.
RNA-Binding; Nuclear protein; Phosphorylation.
RNA-BINDING (RRM)
DOMAIN 111 187
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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           modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                             the
                                                                                                                                                                                                                                        detection of species-specific 
Sene 126:265-268(1993).
                                                                                                                                                                                                                                                                                        MEDLINE=93246255; PubMed=7916708;
Semsei I., Troester H., Bartsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005634; C:nucleus;
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                                                                                                                                                                                                                                                                                                                                                                                                        homolog)
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                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
                                                                                                          SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                       FUNCTION: La protein plays a role in the transcription of polymerase III. It is most probably a transcription termin factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precurse of RNA polymerase III transcripts including tRNA and 4.58.
                                                                                                                                                               and 7-2 RNAs.
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(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
otein homolog (La ribonucleoprotein)
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Rodentia;
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Pred. No.
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RESULT 12

LA_HUMAN P05455;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Robestein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Robestein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Robestein M.J., Wadin T.B., John M., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., L.J., Males S., Garcia A.M.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willialon D.K., Wazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Willialon D.K., Wazny D.M., Sodergren E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
RA Rodriguez A.C., Shevchmats M.J., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
RA Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1989 (Rel. 11, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
Lupus La protein (Sjogren syndrome typ
                                                                                                                                   SEQUENCE OF 54-97 FROM N.A. MEDLINE=85166283; PubMed=3856888;
                                                                                                                                                                                                                                                      Sturgess A.D.,
Coppel R.S.;
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Chan E.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
sequences for RNA-binding";
Nucleic Acids Res. 17:2233-2244(1989).
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Mammalia; Eutheria;
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MEDLINE=89251617;
                                                       Proc.
                                                                       antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89053970; PubMed=3192525;
Chambers J.C., Kenan D., Martin H
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                                                                                              'Isolation
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Res. 17:2233-2244(1989)
                                                                                                                     Keene J.D.
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ivan K.F., Tan E.M.;
                                                         Sci.
PubMed=2470590
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                                                         82:2115-2119(1985)
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Query Match
Best Local Similarity
                                                                                                                     Pfam; PF05383; La; 1.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; La; 1.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS50102; RRM RNP 1; 1.
SYStemic lupus erythematosus; R
                                                         DOMAIN
MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22346609; PubMed=12458796;
Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S
Van Venrooij W.J., Pruijn G.J.M.;
"The human La (SS-B) autoantigen interacts with DDX15/hPrp43,
putative DEAH-box RNA helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Göttlieb E., Steitz J.A.; Function of the mammalian La transcription termination by FEMBO J. 8:851-861(1989).
                                                                                                                                                                                                                                             InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                             GO; GO:0030529; C:ribonucleoprotein complex; TAS GO; GO:00003729; F:mRNA binding; TAS. GO:0000049; F:tRNA binding; TAS. GO; GO:00008334; P:histone mRNA metabolism; TAS.
                                                                                                                                                                                                                                                                                                                                                                                           PIR; A31888; A31888.
Genew; HGNC:11316; S
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC001289; AAH01289.1; -. EMBL; BC020818; AAH20818.1; -.
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                                                                                                                                                                                                                                                                                                GO; GO:0006400; P:tRNA modification;
                                                                                                                                                                                                                                                                                                                                                                              MIM; 109090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8:1428-1443(2002).

FUNCTION: La protein plays a role in the transcription termination polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent factor. Binds to the 3' termini of virtually all nascent for polymerase III transcripts. It is associated with precursor for polymerase TII transcripts including tRNA and 4.5S, 5S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and 7-2 RNAs.
SUBUNIT: Interacts with DDX15.
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: PHOSPHORYLATED. THE PHOSPHORYLATION
C-TERMINAL PART OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               often contain antibodies that react with the normal cellul La protein as if this antigen was foreign. SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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                                                                                                       protein.
                                                           408
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366
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           46.3%;
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RNA polymerase III.";
                                                         RNA-BINDING (RRM).
PHOSPHORYLATION (BY CK2).
EC153C15F9187FC4 CRC64;
             No 44
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gen on serine
             11;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Ballew R.C., Rogers Y.-H.C., Blazef G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gery J.M., Cawley S., Dahlke C., Davenport L.B., Dovies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebbios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krevitz S., Kulp D., Lai Z.,
RA Mcikulov G., Milshina N.V., Mobarry C., Morris J., Moshreti A.,
RA Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Releb J.M.,
RA Molson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Staden-Kiamos I., Simpson M., Stupski M. P., Smith T.,
RA Shue B.C., Staden-Kiamos I., Simpson M., Stupski M. P., Smith T.,
RA Sylerskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Harliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Zhang M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Zhong W., Zhang S., Zha X., Smith H.O.,
RA Gibbs R.-, Shan M., Stupski M. P., Smith H.O.,
RA Gery R. R., Shan M., Shan M., Shan S., Zhao Q., Zheng L.,
RA Gery R. R., Shan M., Shan M., Shan S., Zhao 
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                              REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                             modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: May play a key role in transcriptional regulator.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PTM: The N-terminus is blocked.
                                                                                                                       DOMAIN
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                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Oocyte specific DEVELOPMENTAL STAGE: Expressed at a
                                                                                                                                                                                                                                            A56678; A56678
                                                                                                                                                                                                                                                            AE003768; AAF56858.2; -.
                                                                                                                                                                                                                                                                                 X63503; CAA45074.1;
                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                   protein; DNA-binding;
                                                                                                                                                                                                                       FBgn0005596; yem-alpha.
                                       AA;
                                                                                                                                                                                                                                                                                                                                      institutions as long as its content is in no way attement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
  47.48;
                                         109310 MW;
    Score 45;
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ASP/GLU-RICH (ACIDIC)
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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Matches 9; Conserv
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                                                                                                       Query Match
Best Local :
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P10881;
01-JUL-1989
01-JUL-1989
28-FEB-2003
                                                                                                                                                                                   PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; 1.
RNA-binding; Nuclear protein; P
DOMAIN
11 187
RN
SEQUENCE 404 AA; 46534 MW;
                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBUNIT: Interacts with DDX15 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chan E.K.L., Sullivan K.F., Tan E.M.; "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheri
Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lupus La protein homolog (La ribonucleoprotein)
homolog).
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X13698; CAA31986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 17:2233-2244(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences for RNA-binding."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89202037; PubMed=2468131;
Chan E.K.L., Sullivan K.F., Tan E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S03849; S03849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
Similarity 7; Conserv
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                                                                                 Conservative
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Last annotation update)
                                                                                                                                                                                                                  RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                 Score 44;
                                                                                                                                                                                            4EE30B5C262AD6A1
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                                                                                                                                    DB 1;
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                                                                                                                                      Length 404;
                                                                                                                                                                                            CRC64;
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                                                                                    Indels
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                       STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
                                                                                                                                                   Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                   Inorganic pyrophosphatase hydrolase) (PPase).
                                                                                                                                                                                                                                                                                                    28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00719; Pyrophosphatase; 1.
Probom; PD002014; Inorg_pphaph; 1.
ProSTTE; PS00387; PARSE; 1.
PROSTTE; PS00387; PARSE; 1.
Hydrolase; Metal-binding; Magnesium; Complete proteome.
Hydrolase; Metal-binding; Magnesium 1 (BY SIMILARITY).
METAL 72 72 MAGNESIUM 1 AND 2 (BY SIMILARITY).
METAL 104 104 MAGNESIUM 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; G81930; G81930.

HSSP; P17288; 1FAJ.

HAMAP; MF_00209; -; 1.

InterPro; IPR008163; Inorg_pphsph.

InterPro; IPR008162; Pyrophosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL162754; CAB84132.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitidis Z2491.";
Nature 404:502-506(2000).
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SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM
                                                                                                                                                                                                  Neisseria meningitidis
                                                                                                                                                                                                                                 PPA OR NMB0641.
                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       PYR_NEIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Diphosphate + H(2)0 = 2 phosphate. CORACTOR: Binds 4 magnesium ions per subunit. Other metal ions can support activity, but at a lower rate. Two magnesium ions are required for the activation of the enzyme and are present before substrate binds, two additional magnesium ions form complexes with substrate and product (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the PPase family.
                                                                                                                         _TaxID=491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLPQQLIKQIEFHFNH 141
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72
104 1
177 AA;
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(Rel. 42, Last annotation update)
(ronhosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
                                                                                                                                                                                                                                                                                                                                                (Re1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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N.J., Heidelberg J.,
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Pred. No. 3.3;
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  (See http://www.isb-sib.ch/announce/
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  Jeffries A.C.,
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Best Local
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P25992; Q9VAP4;
01-MAY-1992 (Rel
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ProDom; PB002014; Inorg_phsph; 1.
PROSITE; PS00387; PPASE; 1.
PROSITE; PS00387; PPASE; 1.
Hydrolase; Metal-binding; Magnesium; Complete proteome.
Hydrolase; Metal-binding; Magnesium 1 (By SIMILARITY).
METAL 72 72 MAGNESIUM 1 AND 2 (BY SIMILARITY)
METAL 72 72 MAGNESIUM 1 (BY SIMILARITY).
METAL 104 104 MAGNESIUM 1 (BY SIMILARITY).
SEQUENCE 177 AA; 19811 MW; 6017182C446A8567 CRC64;
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           "The
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
             Ait-Ahmed O., Bellon B., Capri M., Joblet C., Thomas-
"The yemanuclein-alpha: a new Drosophila DNA binding
                                             STRAIN=Canton-S;
MEDLINE=92297435; PubMed=1606021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAWAP, MF 00209; -; 1.
InterPro; IPR008163; Inorg_pphsph.
InterPro; IPR008162; Pyrophosphatase.
Pfam; PF00719; Pyrophosphatase; 1.
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TIGR; NMB0641; -.
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                                                                             SEQUENCE FROM
                                                                                                           NCBI_TaxID=7227;
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substrate binds, two additional magnesium ions form
substrate and product (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the PPase family.
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Pred. No. 3.
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3.3;
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H., Clark E.B.,
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Note=No experimental confirmation available; SIMILARITY: Contains 6 cadherin domains.

IsoId=Q9Y5H7-3; Sequence=VSP_008704, VSP_

IsoId=Q9Y5H7-2;

Sequence=VSP_000679,

VSP_000680

008705;

EMBL; AF152313; AAD43707.1; -.
EMBL; AF152483; AAD43744.1; -.
EMBL; AF05609; AAD43731.1; -.
EMBL; BC033735; AAH33735.1; -.
EMBL; BC037785; AAH37785.1; -.

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Best Local S
Matches 8
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REPEAT
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DOMAIN
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TRANSMEM
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PROSITE; PSS00232; CADHERIN_2; 6.
PROSITE; PS50268; CADHERIN_2; 6.
Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
Calcium-binding; Cell adhesion; Multigene family.
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VARSPLIC
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DOMAIN
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DOMAIN
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SIGNAL
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                                                                                                                                                                                                                                                                                                 InterPro; IPR002126; Cadherin.
Pfam; PF00028; cadherin; 5.
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                               Score 48; I
Pred. No. 5.
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Missing (in isoform 2).
/FTId=VSP_000680.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
PROPNPDWRYSASLRAGWHSSVHLEEAGILRA ->
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                                                                           FTId=VSP
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                                                 issing (In isoform 3).
FTId=VSP_008705.
-> S (IN REF. 3).
7143EECE1A357CD6 CRC64;
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5.7;
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RESULT 7
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Q9JVG3;

28-FEB-2003

28-FEB-2003

10-OCT-2003
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Pardigon N., Strauss J.H.;
Pardigon N., Strauss J.H.;
"Mosquito homolog of the La autoantigen binds to Sindbis VI.
"Mosquito homolog of the Ja autoantigen binds to Sindbis VI.
"Mosquito homolog of the Ja autoantigen binds to Sindbis VI.
"Mosquito homolog of the Ja autoantigen binds to Sindbis VI.
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Q26457;
15-JUL-1998
15-JUL-1998
                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrohydrolase) (PPase)
PPA OR NMA0851.
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La
Redes albopictus (Forest day mosquito).
Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIMA
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PROSITE; PS00030; RRM RNP 1; FALSE NEG.
RNA-binding; Nuclear protein; DNA-binding.
RNA-BINDING (
DOMAIN 141 228 RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EWBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for compatities requires a license agreement (See http://www.isb-sib.ch/ananatics.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amounts are present in the cytoplasm.
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain
-!- SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymerase III. Binds RNA and DNA. Binds to the 3' end of the minus strand of Sindbis virus RNA. This may be significant for Sindbis virus RNA replication.

-i- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=96135233; PubMed=8551578;
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NCBI_TaxID=7160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
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                                                                                                                Neisseria meningitidis (serogroup A)
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8; Conserv
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IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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80.0%;
                                                                              Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; I
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4E5CC8F21C40F452 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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) (Pyrophosphate phospho-
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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Best Local
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CONFLICT
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10-OCT-2003 (Rel. 42, Last annotation update)
SWI/SNF related, matrix associated, actin dependent r
chromatin subfamily B member 1 (Integrase interactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Z0H3;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000 MIM
                    MGD; MGI:1328366; Smarcb1.
InterPro; IPR006939; SNF5.
Pfam; PF04855; SNF5; 1.
                                           EMBL; AJ011740; CAA09761.1;
EMBL; AJ011739; CAA09760.1;
MGD; MGI:1328366; Smarcb1.
                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                This
                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                           Biochem.
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99225325; PubMed=10208879; Bruder C.E., Dumanski J.P., Kedra D.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMARCB1 OR SNF5L1 OR INI1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04855; SNF5; 1.
Transcription regulation; Activator; Nuclear Alternative splicing; Anti-oncogene.
VARSPLIC. 69 77 Missing (in isof
           Transcription regulation; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                     forms.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (mSNF5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                       IBOId=Q9Z0H3-2; Sequence=VSP 004400; SIMILARITY: Belongs to the SNF5 family
                                                                                                                                                                                                                                                               access their targets.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0005654; C:nucleoplasm; TAS.
GO:0015074; P:DNA integration;
GO:0006357; P:regulation of trai
                                                                                                                                                                                                               Name=A; Synonyms=INIIA;
IsoId=Q9Z0H3-1; Sequence=Displayed;
Name=B; Synonyms=INIIB;
                                                                                                                                                                                                                                                                                                  FUNCTION: Involved in chromatin-remodeling. Part of a complex that opens the chromatin to facilitate the transcriptional machinery to
                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                               mouse ortholog of the human SMARCB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256
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378
382
385 /
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382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VSP_004399.
S -> P (IN REF. 2).
L -> E (IN REF. 3).
G -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                    A AND B).
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                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                           257:886-890(1999)
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                                                                                                                                                                                                                                                                                                                                                  encodes
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RESULT
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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max. R.L., Waing J., Hsieh F.,
RA Diacchenko L., Marusina K., Farmer AA., Rubin G.M., Hong L.,
RA Diacchenko L., Marusina K., Farmer AA., Rubin G.M., Hong L.,
RA Diacchenko L., Marusina K., Farmer AA., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Butkerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
"In human and mouse cDNA sequences.",
L. FWINGTION. Optential calcium.denondent cell-adhesion protein. May
L. L. FWINGTION. Optential calcium.denondent cell-adhesion protein. May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu Q., Maniatib i.,
"A striking organization of
"A striking organization of
like cell adhesion genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Y5H7, O75284; Q8N4R3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Protocadherin alpha 5 precursor (PCDH-alpha5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subramanian S., Martin C.H.; "Sequencing of human chromosome 5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimmerly W., Bondoc M., Cheng J.,
Kadner K., Miguel T., Miller C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
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                                                   SUBCELLULAR LOCATION: Type ALTERNATIVE PRODUCTS:
                                                                                                      FUNCTION: Potential calcium-dependent cell-adhes be involved in the establishment and maintenance
                                                                                       neuronal connections in the brain.
                                   Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
   IsoId=Q9Y5H7-1;
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9; Conserv
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Sequence=Displayed
                                  splicing; Named isoforms=3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform B).
/FTId=VSP_004400.
B7BCA26875BD943D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              large family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                       membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pitluck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Connolly K. Pitluck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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                                                                                                       cell-adhesion maintenance of
                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .S., Gunning Pollard M.,
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                                                                     (Ву
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                                                                       similarity)
                                                                                                       protein.
specific
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Rojeski H.,
                                                                                                                                                                                                                                                                                                             fullahy S.J., ratne P.H., Hulyk S.W.,
                                                                                                                                                                                                                                                                              Sanchez A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 4
SNF5_HUMAN
ID SNF5_HUMAN
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
RA Sher E.K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
CC polymerase III. Binds RNA and DNA. Binds to precursors of RNA
CC polymerase III transcripts. May play a specialized role during fly
                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                           Matches
                                                                                                                                                                                                                                            CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0011638; La.
GO; GO:0008098; F:5S rRNA primary transcript binding;
GO; GO:0003723; F:RNA binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003666; AAF53885.1; -. PIR; A53773; A53773. PIR; A53781; A53781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U07652; AAA20518.1; -. EMBL; L32988; AAA21776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                               RNA-binding;
                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50102; RRM; 1. PROSITE; PS00030; RRM_RNP
                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glands.
- SIMILARITY: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pupal, and adult development. Expression throughout the embryo is followed by a restricted pattern of mesodermal expression that is later confined to the visceral mesoderm, gonads, gut, and salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               later confined to the visceral
                                                                                          51
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                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              PR00302;
                                                                                                                    DORIIKQLEYYFGN
                                                                                          ERAIIRQVEYYFGD
                                                                                                                                                                                                                         329
390
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182
283
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                               Nuclear protein;
                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                    LUPUSLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAGE: Expressed throughout
                                                                                                                                                                                                                                            169
183
283
329
                                                                                                                                                                                                                              44884 MW;
                                                                                                                                                                         52.6%;
                                                                                          64
                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA recognition motif (RRM) domain.
                                                                                                                                                           5
                                                                                                                                                                         Score 50; 1
Pred. No. 1
                                                                                                                                                                                                                                            A -> T (IN REF. 1).

KH -> NS (IN REF. 1).

A -> R (IN REF. 1).

K -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                               DNA-binding RNA-BINDING (RRM)
                                                                                                                                                                                                                              A8099288B90446A5 CRC64;
                                                                                                                                                             Mismatches
       385
                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gonads, gut, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                embryonic,
                                                                                                                                                           <u>'</u>
                                                                                                                                                                                            Length 390;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                larval,
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EMBL;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
301/SNF related, matrix associated, actin dependent regulator chromatin subfamily B member 1 (Integrase interactor 1 protein (hSNF5) (BAF47).
                                          EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way nodified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 394:203-206(1998).

-|- FUNCTION: Involved in chromatin-remodeling. Part of a complex that opens the chromatin to facilitate the transcriptional machinery to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE MEDLINE=99225325; PubMed=10208879; Bruder C.E., Dumanski J.P., Kedra D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    access their targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Versteege I., Sevenet N., Lange J.,
Handgretinger R., Aurias A., Delattr
"Truncating mutations of hSNF5/INI1
Nature 394:203-206(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=98334382; PubMed=9671307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalpana G.V., Marmon S., Wang W., "Binding and stimulation of HIV-1
                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yeast transcription factor SNF5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMARCB1 OR SNF5L1 OR INI1.
                                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             torms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The mouse ortholog of the human SMARCB1 gene encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95099327; PubMed=7801128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
L; AJ011738; CAA09759.1; ALT_SEQ.
L; Y17118; CAA76639.1; ALT_SEQ.
L; Y17119; CAA76639.1; JOINED.
L; Y17120; CAA76639.1; JOINED.
L; Y17121; CAA76639.1; JOINED.
L; Y17122; CAA76639.1; JOINED.
L; Y17123; CAA76639.1; JOINED.
L; Y17124; CAA76639.1; JOINED.
L; Y17125; CAA76639.1; JOINED.
L; Y17126; CAA76639.1; JOINED.
L; Y17126; CAA76639.1; JOINED.
L; Y17126; CAA76639.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the SNF5 family. DATABASE: NAME=Atlas Genet. Cytogenet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWW="http://www.infobiogen.fr/services/chromcancer/Genes/SMARCB11D169.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
Name=A; Synonyms=INI1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HIV-1) integrase in
                                                                                                                                                                                                                              U04847; AAA81905.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266:2002-2006(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Commun.
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1., Delattre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257:886-890(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0:
                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunodeficiency virus-type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncol. Haematol.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN MALIGNANT RHABDOID
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in homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gulator of protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ဝှု
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Best Local
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LAB XENLA
P28049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding;
DOMAIN 1
DOMAIN 1
DOMAIN 3
SEQUENCE 42
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
Pfam; PF00076; rrm; 1.
PR.NITS; PR000715; LA; 1.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata
Eukaryota; Batrachia; Anura;
Amphibia; Batrachia; Anura;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                               expression.";
J. MOL. Biol. 231:196-204(1993).

-I- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts (By similarity).
-I- SUBCELLUIAR LOCATION: Nuclear (Probable).
                                                                                        InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                         the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scherly D., Stutz
"La proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homolog B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23,
01-AUG-1992 (Rel. 23,
15-MAR-2004 (Rel. 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93287095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lupus La
                                                                                                                                                                                                                                                               PTM: Phosphorylated (Probable).

MISCELLANEOUS: There are two forms of La, LaA and I SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.

SIMILARITY: Contains 1 RNA recognition motif (RRM)
                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly constant steady state level in mature occytes, eggs, and earl
                                                                                                                               ; X68818; CAA48716.1; -. S33817; S33817.
                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       004 (Rel. 43, Last protein homolog B
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428 AA;
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F., Lin-Marq N.,
Xenopus laevis.
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ear_protein; F
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56.2%;
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                  RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Ferriera S., Fleischmann W.,
RA Choston K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Choston K., Doup T.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liak X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Markell M., Mattei B., Wallahian W.,
Markell M., McIntosh T.C., McLeod M.P., McPherson D.,
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01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburnar R.A., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani B., An H.-J., Andrews-Pfannkoch C., Baldwin D., Bald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
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DOMAIN 10 202 RNA-BINDING (RRM).

DOMAIN 315 331 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bai C., Li Z., Tolias P.P.;
"Developmental characterization of a Drosophila RNA-binding protein
homologous to the human systemic lupus erythematosus-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Canton-S; TISSUE=Ovary; MEDLINE=94309632; PubMed=8035794;
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LA OR CG10922.
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Cell. Biol. 14:5123-5129(1994).
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   Milshina N.V., Mobarry
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constant steenbryos	EUKATYOTA; METAZ Amphibia; Battrac Xenopodinae; Xen NCBI_TAXID=8355; [1] SEQUENCE FROM N. TISSUE=Oocyte; MEDLINE=93287095 Scherly D., Stut "La proteins fro "La proteins fro "La proteins fro "Appression."; "Appression	LT 1 XENLA LAA XENLA P28048; 01-AUG-1992 01-AUG-1992 15-MAR-2004 Lupus La pro LaAI. LAAI. XENDAN XENDAN XENDAN XENDAN LAAI.	4444666 10000000000000000000000000000000
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mbryos. INCELLANEOUS: There are two forms of LISCELLANEOUS: The SAMMALIAN LA PROTE: SWISS-PROT entry is copyright. It is pure the swiss Institute of Bioinformat: LINCOME and LISCELLANEOUS: The Samma is long of the swiss Institute of Bioinformat: License allocation as long of the statement is not removed. License arequires a license agreement (See lend an email to license agreement see lend an email to license agreement	Chordata; Craniata; Anura; Mesobatrachi . Anura; Mesobatrachi . Lin.Marq N., Clark . Lin.Marq N., Clark . Clark . Clark chopus laevis. cDNA c 6-204 (1993) . Lin. Marg n. cle in It is most probably . the 3' termini of v . ranscripts (By simil ITION: Nuclear (Proba AGE: Barely detectab . age III/IV oocytes,	ALIGN PRT; ted) sequence sequenti Annotati (La ribon (La ribon)	RPOC MYCGE Y165 UREPA DGT1 THETN SYM RHILO SYM BORBU DNAK STRGR TRNL CANAL NUT1 YEAST RBS CYAPA RBS GUITH RBSA SOLTU RBSB_SOLTU
level in mature occytes, eggs, and probable). are two forms of La, LaA and LaB, in MANWALIAN LA PROTEIN. 1 RNA recognition motif (RRM) domain copyright. It is produced through a ute of Bioinformatics and the EMBI cs Institute. There are no restrictivations as long as its content is int is not removed. Usage by and its eagreement (See http://www.isb-siluseagisb-sib.ch). 18 La. 18 La. 19 Tec_mot.	a; Pipoid a; Pipoid son S.G.; loning ar loning ar transcr the trar a transcr irtually arity). le in sta then exhi	AA. AA. te) date) oprotein A)	COR SOR SOR SOR SOR SOR SOR SOR SOR SOR S
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early n xenopus. n. collaboration cutions on its s in no way for commercial b.ch/announce/	Б	Ħ	mycoplasma ureaplasma thermoanaer rhizobium 1 borrelia bu streptomyce candida alb saccharomyc cyanophora guillardia guillardia solanum tub solanum tub

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adenine/cytosine DNA methyltransferase - Helicobacter pylori (strain 26695)
c;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: F64526
C;A
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jun-2002
C;Accession: A56678; S22146
R;Ait-Ahmed, O.; Bellon, B.; Capri, M.; Joblet, C.; Thomas-Delaage, M.
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A;Experimental source: serogroup
C;Genetics:
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A;Introns: 80/3; 154/3; 428/1 477/2; 557/2
C;Keywords: DNA binding; oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1002 < AIE>
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A;Title: The yemanuclein-alpha: a new Drosophila DNA binding protein specific
A;Reference number: A56678; MUID:92297435; PMID:1606021
A;Accession: A56678
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A; Residues: 1-177 < PAR>
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                                                                                                                     ;Residues: 1-823 <TOM>
;Cross-references: GB:
                                                                                                                                                                             Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA
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Best Local
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                                                                                                                     GB:AE000527; GB:AE000511; NID:g2313131; PIDN:AAD07124.1; PID:g23131:
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52.9%;
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Score 44.5; D
Pred. No. 41;
6; Mismatches
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42;
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A;Status: preliminary
A;Molecule type: DNA
A,Residues: 1-300 <KUR>
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-158 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76535.1; PID:g17133973; GSPDB:GN00179
A;Cross-references: GR:BA000019; PIDN:BAB76535.1; PID:g17133973; GSPDB:GN00179
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C;Accession: AD2410
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nikazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Yasuda, M.; Yasuda
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A;Map position: linear chromosome
C;Superfamily: probable transcription regulator lsyR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription regulator, LysR family Atu4437 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AI3101
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A;Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana.
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2410
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                                                                              3 ADQRIIKQLEYYFGN 17
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Pred. No. 17;
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McClell,
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89777
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H89777
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A;Title: A human protein with homology to Saccharomyces cerevisiae A;Reference number: $54705; MUID:9528318; PMID:7739891
A;Accession: $54705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: Integrase Interaction (man) (c;Species: Homo sapiens (man) (c;Species: Homo sapiens (man) (c;Date: 27-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999 (c;Date: 27-Oct-1995 #seroe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capsular polysaccharide synthesis enzyme Cap5P [imported] - Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-135,'S',137-385 <KAL>
A;Cross-references: GB:U04847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 266, 2002-2006, 1994
A;Title: Binding and stimulation of HTV-1 integrase by a human homolog
A;Reference number: A55388; MUID:95099327; PMID:7801128
A;Accession: A55388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. R;Kalpana, G.V.; Marmon, S.; Wang, W.; Crabtree, G.R.; Goff, S.P. Science 266, 2002-2006, 1994
                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-391 <KUR>
A;Cross-references: GB:BA000018; PID:g13700080; PIDN:BAB41379.1; GSPDB:GN00149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: cell line HL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                             A; Experimental
                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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                                                                                     Query Match
Best Local S
Matches 8
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                                                                                                                                                                               Superfamily:
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Best Local
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  ASRRICEAIEYYFG 376
                                         ADORIIKQLEYYFG 16
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                                                                                                                                                                                                                                             source: strain
                                                                                       Conservative
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57.1%;
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Pred. No.
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A; Experimental source: serogroup
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                         A; Cross-references: GB: AE001862;
A; Experimental source: strain R1
                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-156 < WHI>
                                                                                                                                                                                                                                                                                                       A; Title: Genome sequence of A; Reference number: A75250; A; Accession: D75605
                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                         C; Genetics:
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                                                                                                                                                   A; Map position: 2
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Best Local
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                                 DDADQRIIKQLEYYFGN 17
EDADQTALNQLQYAYVN
                                                                         Conservative
                                                                                           47.48;
47.18;
                                                                                                                                                                                                                                                                                                                               the radioresistant bacterium Deinococcus radiodurans MUID:20036896; PMID:10567266
                                                                           4.
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                                                                                             Score 45;
Pred. No.
                                                                             Mismatches
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                                                                                                             Length 156
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: F81175
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A., ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: F81175
A;Accession: F81175
A;Accession: F81175
A;Residues: 1-177 - TET> A;Accession: CETANONALS. OFF.AERONALS. NITH. G7725863. DIDN:AAFA1064 1: PID:G722586
A;Residues: 1-177 - TETANONALS. GR.AERONALS. NITH. G7725863. DIDN:AAFA1064 1: PID:G722586
A;Residues: 1-177 - TETANONALS. GR.AERONALS. NITH. G7725863. DIDN:AAFA1064 1: PID:G722586
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A;Residues: 1-177 - TETANONALS. NITH. G7725863. DIDN:AAFA1064 1: PID:G722586
A;Residues: 1-177 - TETANONALS. NITH. G7725863. DIDN:AAFA1064 1: PID:G722586
A;Residues: 1-177 - TETANONALS. NITH. G7725863. DIDN:AAFA1064 1: PID:G722586
A;Residues: 1-177 - TETANONALS. NITH. G7725863
A;Residues: 1-177 - TETANON inorganic pyrophosphatase NMB0641 [imported] - Neisseria meningitidis (strain MC58 serog C;Species: Neisseria meningitidis 10 GB:AE002098; NID:g7225863; PIDN:AAF41064.1; PID:g72258

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                                                                      A;Gene: NMB0641
C;Superfamily: inorganic pyrophosphatase
                                   Matches
                                                    Query Match
                                           Local Similarity
                2 DADQRIIKQLEYYFGN 17
                                   Conservative
                                           47.48;
                                   6,
                                           Score 45;
Pred. No.
                                   Mismatches
                                            σ
                                                     DB 2;
                                   ω
                                                    Length 177
                                    Indels
                                   0
                                    Gaps
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R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Nature 404, 502-506, 2000 probable inorganic diphosphatase (EC 3.6.1.1) NMA0851 [imported] - Neisseria C;Species: Neisseria meningitidis C;Data: 05-May-2000 #sequence_revision 05-May-2000 #text_change 03-Jun-2002 C;Accessin: G81930 G81930 RESULT 11 S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.;

DNA sequence of

a serogroup A strain of Neisseria menigitidis Z2491.

S.R.; More

meningitid

21-Jul-2000

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Gaps

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ribonucleoprotein La.B - African clawed frog
ribonucleoprotein SS-B - African clawed frog
RS-BL1ernate names: autoantigen SS-B/La; ribonucleoprotein SS-B - C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Datcession: S33817; S28544
                                                                                                                                                                             A;Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212854
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X:, Kaul, S:, Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon,
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Eraser, C.M.; Venter
enss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                               hypothetical protein At2943970 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F6B13.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00677; G84872
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A;Reference number: Z14180
A;Accession: T0677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.

J. Mol. Biol. 231, 196-204, 1993

A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.

A;Reference number: S33817; MUID:93287095; PMID:8510143

A;Accession: S33817
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F;228-428/Domain:
                                                                                       Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: AB4420; MUID:20083487; PMID:10617197
A;Accession: GB4872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876 C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-427 < SCH>
  A;Cross-references: GB:AE002093;
                          A;Molecule type: DNA
A;Residues: 1-529 <STO>
                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-529 < ROU>
                                                                                                                                                                                                                                                                                                                                            Status: translated from GB/EMBL/DDBJ
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phosphorylated #status predicted <PHY>
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56.2%;
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NID:g3212854; PIDN:AAC23405.1; GSPDB:GN00139
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Pred. No. 0.18;
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Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: A;Reference number: A53781; MUID:94309661; PMID:8035818
A;Accession: A53781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-390 <BAI>
A;Cross-references: GB:U07652; NID:g464019; PIDN:AAA20518.1; PID:g464020
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Bai, C.; Li, Z.; Tolias, P.P. Mol. Cell. Biol. 14, 5123-5129, 1994
Mol. Cell. Bevelopmental characterization of a Drosophila A;Reference number: A53773; MUID:94309632; PMID:8035794
A;Accession: A53773
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R;Yoo, C.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_c
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: leucine zipper; RNA binding
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A;Map;position: 2
A;Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3
                                                                                                                                                                                                                             A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                               A;Gene: FlyBase:La
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A; Residues: 1-390 < YOO>
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C;Date: 13-Jan-1995 #sequence_revision
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Pred. No.
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Pred. No. 0.
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Pred. No. 2
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20-Sep-1999

a yeast <u>.</u>.

Gaps

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Gaps

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Title: Perfect score: Run on: OM protein - protein search, using sw model US-09-836-073-17 95 September 10, 2004, 17:33:11; Search time 14.0782 Seconds (without alignments)
122.988 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

Scoring table: Sequence: BLOSUM62 1 DDADQRIIKQLEYYFGNI 18

Searched: 283366 seqs, 96191526 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Listing

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	A26459	A89798	S45634	F90570	S73653	T27669	A70183	G64049	G95104	JC1494	A31888	S03849	G97972	A96185	AI3101	AD2410	F64526	A56678	G81930	F81175	D75605	H89777	S54705	A53781	A53773	T00677	S33817	S33818	T30953	ID
	helix-destabilizin	hypothetical prote	adenylate kinase (hypothetical prote			hypothetical prote	нì	hypothetical prote	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	conserved hypothet	probable transcrip	transcription regu	hypothetical prote	adenine/cytosine D	yemanuclein-alpha	probable inorganic	inorganic pyrophos	hypothetical prote	capsular polysacch	transcription fact	ribonucleoprotein	La/SS-B homolog D-	hypothetical prote	ribonucleoprotein	ribonucleoprotein	hypothetical prote	Description

A; Molecule type: mRNA A; Residues: 1-428 <SCH1 A; Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874 A; Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874 C; Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor. C; Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C; Keywords: phosphoprotein; RNA binding C; Keywords: phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology <RRM>

most of which

F;113-118/Region: RNA-binding RNP2 motif

ribonucleoprotein La.A - African clawed frog
ribonucleoprotein La.A - African clawed frog
RyAlternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03.7eb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: S33818; S28545
R;Scherly, D.; Stutz, F; Lin-Marq, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
J. Mol. Biol. 231, 196-204, 1993
A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Reference number: S33817; MUID:93287095; PMID:8510143

hypothetical prote puatative sulfatas	161331		400		#	Ü
hypothetical prote puatative sulfatas	731031	د	100	3		•
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	F65012	ب	361	43.2	41	ü
acyl carrier proce	G90199	N	350	43.2	41	2
hypothetical proce	S76647	N	346	43.2	41	Ξ
neme oxygenase (de	A35199	بر	315	43.2	41	6
RNA-binding procei	T43542	N	298	43.2	41	9
rna binding procei	T38937	N	298	43.2	41	8
adenylate kinase (G90582	N	214	43.2	41	7
hypothetical proce	S75273	1	192	43.2	41	6
_	S77850	N	178	43.2	41	ភ
KEXI procein precu	A29651	N	729	43.7	41.5	4.
phospholipase u ra	E97104	N	188	43.7	41.5	ũ
cadnerin - Airican	\$43064	N	905	44.2	42	៊
LIT	IJXLCP	1	895	44.2	42	Ξ
conserved hypothet	B87467	N	840	44.2	42	õ

ALIGNMENTS

Query Match Best Local Similarity Matches 17; Conserva Qy	RESULT 1 T30953 hypothetical protein C4484 C;Species: Caenorhabditis C;Date: 22-Oct-1999 #seque C;Accession: T30953 R;Sammons, L; Wohldmann, submitted to the EMBL Data A;Description: The sequence A;Reference number: Z20945 A;Accession: T30953 A;Status: preliminary; tra A;Molecule type: DNA A;Residues: DNA A;Residues: 1-396 <sam- 1,114="" 3="" a;cross-references:="" a;experimental="" a;note:="" c4484.4="" c;genetics:="" c;superfamily:="" embl:a="" ribonucleop<="" source:="" str="" th=""></sam->
	RESULT 1 T30953 C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Alace: 22-Oct-1999 #sequence_revision 2 C;Accession: T30953 R;Sammons, L.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, Augu A;Description: The sequence of C. elegan A;Reference number: Z20945 A;Accession: T30953 A;Status: preliminary; translated from G A;Molecule type: DNA A;Residues: 1-396 <sam> A;Residues: 1-396 <sam> A;Residues: T30953 A;Residues: T30953 A;Rosidues: 1-396 <sam> A;Residues: T30953 A;Rosidues: 1-396 <sam> A;Residues: T306-XSAM A;Residues: 1-396 <sam> A;Cross-references: EMBL:AF003140; PIDN: A;Gross-references: EMBL:AF003140; PIDN: A;Gross-references: EMBL:AF003140; PIDN: C;Genetics: A;Map position: I A;Introns: 45/1; 114/3 A;Note: C44E4.4 C;Superfamily: ribonucleoprotein La; rib</sam></sam></sam></sam></sam>
96.8%; Score 92; DB 2; 1 94.4%; Pred. No. 2.8e-07; Elve 1; Mismatches 0 EYYFGNI 18 EYYFGNI 27	RESULT 1 730953 C;Bpecies: Caenorhabditis elegans C;Apte: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000 C;Accession: T30953 R;Sammons, L; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, August 1999 A;Description: The sequence of C. elegans cosmid C44E4. A;Reference number: Z20945 A;Accession: T30945 A;Accession: T30953 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-396 <sam'> A;Residues: 1-396 <sam'> A;Residues: 1-396 <sam'> A;Resperimental source: strain Bristol N2; clone C44E4 C;Genetics: A;Map position: I A;Introns: 45/1; 114/3 A;Note: C44E4.4 C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology</sam'></sam'></sam'>
. 6	is elegans ot-1999 #text_ legg Dsmid C44E4. MBL/DDBJ Jane C44E4
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Search completed: September 10, 2004, 17:51:53 Job time : 59.4128 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC comprising peptides which comprise a nonclassical cadherin cell adhesion CC recognition (CAR) sequence. The MAS can be used for modulating CC monclassical cadherin mediated functions. They can be used for e.g. CC inhibiting adhesion of nonclassical-cadherin expressing cells in a CC mammal, enhancing delivery of a drug through the skin of a mammal, cenhancing delivery of a drug through the skin of a mammal, companies in a mammal, inhibiting cancer in CC angiogenesis in a mammal, inducing apoptosis in a mammal, stimulating CC expressing cell, preventing or treating obesity in a mammal, stimulating control blood vessel regression in a mammal, enhancing delivery to the CC increasing vasopermeability in a mammal, enhancing drug delivery to the CC increasing vasopermeability in a mammal, enhancing adhesion of conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating synaptic stability in conclassical cadherin-expressing cells, inhibiting synaptic stability in conclassion of foreign tissue in a conclassion of foreign tissue in a conclassion of foreign tissue in
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glitamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                                              31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forension food supplement; medical imaging; diagnostic; genetic disorder
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Tateishi N,
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2001-639362/73
)B; AAS65427.
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2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                              2000US-00540217
2000US-00649167
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                                                                                   Liu C,
                                                                                                                                          INC.
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Pred. No.
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cc sequences. (1) is useful as hybridisation probes, polymerase chain (creaction (PCR) primers, oligomers, and for chromosome and gene mapping, cand in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed (C) in diagnostics as expressed sequence tags for identifying expressed (C) genes. (I) is useful in gene therapy techniques to restore normal (C) expressed in the control of the control of (II) or to treat disease states involving (II). (II) is (II) as (II) and its binding partners are useful in medical imaging (C) sites expressing (II). (I) and (II) are useful in medical imaging (C) sites expressing (II). (I) and (II) are useful for treating disorders (C) polypeptide and polymucleotide sequences have applications in (C) polypeptide and polymucleotide sequences have applications (C) control of genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and (C) amino acid sequences of the invention. Note: The sequence data for this content of the printed specification, but was obtained in (C) electronic format directly from MIPO at the printed specification of the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide sequences. (I) is useful as hybridisation probes,
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polymerase chain
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Query Match
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Matches 8
223
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                               Similarity
8; Conserv
DADEGINKEIVYFFSNL
              DADQRIIKQLEYYFGNI
                                Conservative
                                        50.5%;
239
               18
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                                        Score 48; DB
Pred. No. 30;
                                Mismatches
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                                                Length 650;
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RESULT 15
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AC REPRESENTATION OF THE PROPERTY OF THE PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY64613 standard; peptide; 108
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05-MAY-1998; 06-NOV-1998; 20-JAN-1999; 08-MAR-1999;

98US-00073040. 98US-00187859. 99US-00234395. 99US-00264516.

05-MAY-1999;

99WO-CA000363

11-NOV-1999

Mammalia.

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RESULT 12
AAB95622
ID AAB95
XX AB95
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XX Human
XX Human
XX Homo
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Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                The ini-1 protein may serve an an internal receptor for retrovirus integrase enzymes, and may be responsible for targeting integration to active regions of the chromosome. The ini-1 protein can be expressed in prokaryotic or eukaryotic host cells. It is useful for screening cpds. that disrupt retrovirus (esp. HIV-1) integrase-ini-1 protein interaction and thereby disrupt the retrovirus life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integrase interactor 1; ini-1 gene; antiviral; retrovirus; HIV-1;
human immunodeficiency virus type 1; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 385 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human integrase interactor 1 protein (AAW00081) was identified as the product of the ini-1 gene (AAT34357) isolated from an HL60 cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated integrase interactor-1 gene - used to develop assays for anti-viral agents capable of interfering with integrase interactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT34357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 50-51; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-020286/02
 29-JUL-1999;
                         28-JUL-2000; 2000EP-00116126
                                                                              EP1074617-A2
                                                                                                      Homo sapiens
                                                                                                                                                           Human protein
                                                                                                                                                                                     26-JUN-2001
                                                                                                                                                                                                                                       AAB95622 standard; protein; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP,
                                                                                                                                                                                                                                                                                                      256 DQSDQRVIIKLNIHVGNI 273
                                                                                                                                 primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding.
                                                                                                                                                                                                                                                                                                                               DDADQRIIKQLEYYFGNI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalpana GV;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                     (first entry)
                                                                                                                                                           sequence SEQ ID NO:18340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00248355
                                                                                                                                 detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US006683
  99JP-00248036
                                                                                                                                                                                                                                                                                                                                                                    50.5%;
                                                                                                                                 diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB Pred. No. 16;
                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                  Length 385,
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                          0
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Corynebacterium

glutamicum

Coryneform bacterium; amino acid synthesis; vitamin; organic acid synthesis.

saccharide;

18-DEC-2000; 2000EP-00127688

20-JUN-2001.

C glutamicum protein fragment SEQ ID NO: 5064.

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265

DOSDORVIIKLNIHVGNI

282

0

AAG91310 RESULT 13

AAG91310 standard; protein;

AAG91310;

26-SEP-2001

(first entry)

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Ś
                                                                                                                                                                                                                               length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the

complementary strand of a polynucleotide which comprises one of the 5602

mucleotide sequences defined in the specification, where the

complementary strand of a polynucleotide which comprises as the combination

of an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which comprises a 5'-end

complementary to a combination of a polynucleotide comprising a sequence complementary to a

complementary to a comprise at least 15 nucleotides and the combination of

complementary to a sequence, where the

complementary to a sequence is selected from those defined in the

complementary to a sequence is selected from those defined in the

complementary full-length cDNAs. The primers are useful for synthesising polynucleotides,

particularly full-length cDNAs. The primers are also useful for the

compassing the primer set on the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

complementary in the primer allow obtaining of the full-length

complementary in the primers allow obtaining of the AAH13528 and

complementary without any specialised methods. AAH03166 to AAH13528 and

complementary in the primer set of the above the complementary to a

complementary in the primers and AAH13632 represent

complementary to the primer set of the comprise of the complementary to a

complementary to the comprise of the comprise and complementary to a

complementary to the comprise and the complementary to a

complementary to the comprise and comprise and complementary to a

complementary to the comprise at the comprise and comprise a
                                                       Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1999; 99UP-00300253.
17-AUR-2000; 20000UP-00118776.
02-MAY-2000; 2000UP-00183767.
09-JUN-2000; 2000UP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-318749/34.
                                                                                                                                                             Sequence 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes primer sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 18340; 2537pp + Sequence Listing; English
       DDADQRIIKQLEYYFGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugiyama T,
                                                       Conservative
                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                  50.5%;
                                                       4.
       18
                                                          Score 48; DB
Pred. No. 17;
4; Mismatches
                                                                                       DB
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s for synthesising 5602 full-
Where a primer set comprises
                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K,
C, Otsuki
                                                             <u>ن</u>
                                                                                                          Length 394;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto
                                                               0
                                                             Gaps
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RESULT 9 AAB93709

AAB93709 standard; protein;

376 AA

(first entry) sequence SEQ

ID NO:13301.

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51

:: ||:|:||||: ERAIIRQVEYYFGD

64

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Matches
   Query Match
       Sequence
Local Similarity hes 9; Conserv
Conservative
       Å
  50.5%;
4.
 Score 48;
Pred. No.
Mismatches
    DB 4;
5.
    Length 376;
Indels
0,
Gaps
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0

AAW00081 ID AAW XX

AAW00081 standard; protein; 385 AA

0

RESULT 11

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CC length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the

cc complementary strand of a polynucleotide which comprises one of the 5602

CC nucleotide sequences defined in the specification, where the

cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination

cc of an oligonucleotide comprising a sequence complementary to the

cc complementary strand of a polynucleotide which comprises a 5 -end

cc equence and an oligonucleotide comprising a sequence complementary to a

cc polynucleotide which comprises a 3 -end sequence, where the

cc oligonucleotide comprises at least 15 nucleotides and the combination of

cc oligonucleotide comprises at least 15 nucleotides and the combination of

cc polynucleotide comprises at least 15 nucleotides and the combination of

cc polynucleotide comprises at least 15 nucleotides and the combination of

cc principal comprises at least 15 nucleotides and the combination of

cc particularly full-length cDNAs. The primers selected from those defined in the

cc detection and/or diagnosis of the abnormality of the proteins encoded by

the full-length cDNAs. The primers allow obtaining of the full-length

cc DNAs easily without any specialised methods. AAH03166 to AAH13628 and

cc present human amino acid sequences; and half1362 represent

cc present invertice.

cc present invertices all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13301; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto
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                                                                                                                                                                                                                             CC NAY92331-37 were isolated in a modified yeast two hybrid system using CC NIKI protein as "bait". These are known sequences which are NIK1 CC interacting proteins. The invention concerns purified complexes of a NLK1 CC protein and a NLK1 protein-interacting protein, where the interacting protein is chosen from TrkA, protein phosphatase lalpha, 14-3-3epsilon, CC alpha-tropomyosin, vimentin, p0071, Ini-1, IP-1, IP-2, IP-3, IP-4, or IP-CS. NIK1 (also referred to as Nek2) is a human homologue of the CC aspergillus nidulans mitotic regulator, NIMA kinase. NIK1 is a CC serine/threonine-specific kinase and is thought to play a key role in CC cell-cycle events leading to the onset of mitosis. The complexes, their CC derivatives and NIK1 or NIK1-IP protein and DNA sequences, etc. are CC useful for treating or preventing a disease or disorder involving CC aberrant levels of the complex or protein. Such disorders include cancer, CC hyperproliferative disorders, neurodegenerative disorders (cc cardiomyopathies, viral infections and metabolic disorders
                                                                                            Query Match
Best Local S
Matches 9
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 162-163; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New complex of a NLK1 protein and a NLK1 protein-interacting protein, useful for treating cancer, hyperproliferative disorder, neurodegenerative disorder, cardiomyopathies, viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nandabalan K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIK1 Interacting neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Ini-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY92337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92337 standard; protein; 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA09309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-303742/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200020448-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247
  256
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                                                                                              Similarity 9; Conser
                                                                                                                                                                                          384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQSDQRVIIKLNIHVGNI 264
DQSDQRVIIKLNIHVGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDADQRIIKQLEYYFGNI
                                               DDADQRIIKQLEYYFGNI
                                                                                            50.5%;
llarity 50.0%;
Conservative
                                                                                                                                                                                             A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schulz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US023314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; Ini-1; protein complex; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٧Þ,
  273
                                                 18
                                                                                              Score 48; DB
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                              4;
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                                                                                                                     16;
                                                                                                                                              ω
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                                                                                                 5
                                                                                                                                           Length 384;
                                                                                                 Indels
                                                                                                 <u>,</u>
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                                                                                                 Gaps
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29-JUL-1999; 27-AUG-1999; 11-JAN-2000; 02-MAY-2000;

99JP-00300253. ; 2000JP-00118776. ; 2000JP-00183767. ; 2000JP-00241899.

99JP-00248036

28-JUL-2000; 2000EP-00116126

07-FEB-2001. EP1074617-A2 Homo sapiens Human; primer; Human protein 26-JUN-2001 AAB93709;

Ota

:Isogai T, HELIX RES INST

Nishikawa T,

hikawa T, Hayashi K, S Wakamatsu A, Nagai K,

Sugiyama

Ŧ,

(HELI-)

Claim 8;

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RESULT 7
ABG72119
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Matches
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Best Local :
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21-OCT-1999
22-OCT-1999
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26-OCT-1999
26-OCT-1999
26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
                                                                                                                                                                                                                                        Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide.
                                                                                                                                                                                                                                                                                                                                             ABG72119 standard; peptide; 16
                                                   New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                      Viral replication inhibiting
                                                                                                                                                                                                                                                                                                         28-JAN-2003
                                  Claim 1; Page
                                                                                                           Dasgupta A,
                                                                                                                              (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
                                                                                                                                                                 12-APR-2002; 2002WO-US011589
                                                                                                                                                                                    24-OCT-2002
                                                                                                                                                                                                    WO200283858-A2
                                                                                                                                                                                                                       Drosophila sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -OCT-1999
                                                                                          2003-058634/05
                                                                                                                                                                                                                                                                                                                                                                                            191
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            DDADQRIIKQLEYYFGNI 18
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                           Das
                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                2001US-00836073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0160741P.
99US-0160767P.
99US-0160770P.
99US-0160770P.
99US-0160815P.
99US-0160980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0159331P.
99US-0159637P.
99US-0159638P.
99US-0159584P.
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99US-0161404P
99US-0161405P
99US-0161405P
99US-0161359P
99US-0161350P
99US-0161360P
99US-0161361P
99US-0161920P
99US-0161920P
99US-0161993P
                                   15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0162142P
                                                                                                           S
                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       56.8%;
                                                                                                                                                                                                                                                                                                                                                                                            208
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                      peptide, DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                0
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The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La

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4 DQRIIKQLEYYFGN 17

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RESULT 8
ABB65316
ID ABB6
XX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 8
Query Match
Best Local S
Matches 8
                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL040-ABL16175) and the encoded proteins (ABE7737-ABB77272). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen protein (IAP) in any phase of their life cycle. The peptides of the invention compete with IAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16 AA;
                                                                                                      Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL09419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB65316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 22740; 21pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB65316 standard;
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Similarity
8; Conserv
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57.1%;
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Pred. No.
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                             Score 50;
Pred. No.
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     Mismatches
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                                                        Length 390;
        Indels
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        <u>,</u>
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Best Local S
Matches 8
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
25-MAR-1999
01-APR-1999
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06-APR-1999
16-APR-1999
16-APR-1999
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13-OCT-1999

13-OCT-1999

13-OCT-1999

14-OCT-1999

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14-OCT-1999

14-OCT-1999

21-OCT-1999

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26-OCT-1999

28-OCT-1999

28-OCT-1999

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29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID
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                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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Similarity 44.4%;
8; Conservative
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EDSIQKIVNQVEYYFSDL 13:
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99US-0159294P

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99US-0159330P

99US-0159331P

99US-0159637P

99US-0159637P

99US-0160741P

99US-0160767P

99US-01607767P

99US-0160776P

99US-0160814P

99US-0160814P

99US-0160815P

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99US-0161361P

99US-0161393P

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99US-0161393P
   99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126764P.
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99US-0127462P.
99US-0128734P.
99US-0128734P.
99US-0128734P.
99US-0128777P.
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; Pred. No. 4.4;
7; Mismatches
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16-JUL-1999
19-JUL-1999
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RESULT 5
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Best Local S
Matches
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28-SEP 1999
29-SEP 1999
29-SEP 1999
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21-OCT 1999
22-OCT 1999
  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                       25-FEB-2000;
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                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
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:|: |:|: |:||| ::
EDSIQKIVNQVEYYFSDL 128
                                                                                                                                                                                                                                                                                                                                  standard;
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99US-0156458P

99US-01567117P

99US-01577653P

99US-0158029P

99US-0158029P

99US-0159293P

99US-0159295P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0159637P

99US-0169637P

99US-0160741P

99US-0160770P

99US-0160770P

99US-0160768P

99US-0161358P

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99US-0161393P

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99US-0161393P

99US-0161393P

99US-0161393P
 99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                                                                                                                                                                                                                                                                                                 protein; 923 AA.
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                                                                                                                                                                                                                                             protein
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; Pred. No. 4.4;
7; Mismatches
                                                                                                                                                                                                                                             fragment
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4.4;
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promoter;
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    18-JUN-1999
22-JUN-1999
23-JUN-1999
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26-JUN-1999
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31-JUN
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30-APR 1999;
30-APR 1999;
04-MAY 1999;
06-MAY 1999;
06-MAY 1999;
10-MAY 1999;
11-MAY 1999;
11-MAY 1999;
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12-MAY 1999;
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13-MAY 1999;
14-MAY 1999;
14-MAY 1999;
14-MAY 1999;
15-MAY 1999;
26-MAY 1999;
27-MAY 1999;
28-MAY 1999;
21-MAY 1999;
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
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10-JUN-1999
14-JUN-1999
16-JUN-1999
16-JUN-1999
17-JUN-1999
18-JUN-1999
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07-JUN-1999;
08-JUN-1999;
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21-APR-1999;
23-APR-1999;
23-APR-1999;
99US-0126264P
99US-01274762P
99US-0128734P
99US-013047P
99US-0130510P
99US-0130510P
99US-0132048P
99US-0132485P
99US-0132486P
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99US-013421P
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99US-013945P
99US-0140823P
99US-0142154P
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99US-0140354P. 99US-014083P. 99US-014083P. 99US-0141287P. 99US-0141287P. 99US-014154P. 99US-0142055P. 99US-0142055P.	99US-0139459P. 99US-0139460P. 99US-0139461P. 99US-0139463P. 99US-0139763P. 99US-0139763P. 99US-0139763P. 99US-0139763P.	99US-0137502P. 99US-0138094P. 99US-0138540P. 99US-0138540P. 99US-0139452P. 99US-0139453P. 99US-0139454P. 99US-0139454P. 99US-0139455P. 99US-0139456P. 99US-0139458P.	99US-0132486P. 99US-0132863P. 99US-013256P. 99US-0134218P. 99US-013421P. 99US-0134370P. 99US-0134768P. 99US-0134768P. 99US-0135124P. 99US-013523P. 99US-013523P. 99US-013523P. 99US-013628P. 99US-013629P. 99US-013629P. 99US-013629P. 99US-013629P.	2000EP-00301439. 99US-0121825P. 99US-0123180P. 99US-0123548P. 99US-0126264P. 99US-0126785P. 99US-01267823. 99US-0128234P. 99US-0128234P. 99US-0130077P. 99US-0130449P. 99US-0131449P.
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9US-01 9US-01 9US-01 9US-01 9US-01 9US-01 9US-01	9US-01 9US-01 9US-01 9US-01 9US-01 9US-01 9US-01	903-01 903-01 903-01 903-01 903-01 903-01 903-01 903-01	903-01 903-01 903-01 903-01 903-01 903-01 903-01 903-01 903-01 903-01	99US-0142803P. 99US-0142977P. 99US-0143542P. 99US-0144085P. 99US-0144085P. 99US-0144085P. 99US-0144331P. 99US-0144331P. 99US-0144333P. 99US-0144335P. 99US-0144335P. 99US-0144335P. 99US-0144335P. 99US-0144335P. 99US-01443484P. 99US-0144384P. 99US-01443884P. 99US-01445088P. 99US-0145088P. 99US-01445088P.

Length 18;

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RESULT 2
ABP70526
ID ABP7
XX A
RESULT 3
ABG72115
ID ABG7
XX
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides. The chimeric polypeptides comprise a polypeptide segment that exhibits histone acetyltransferase activity, and a polypeptide segment that exhibits histone acetyltransferase activity, and a polypeptide segment having 40% or greater sequence identity to a subunit of a histone deacetylase chromatin-associated protein complex. The chimeric polypeptides are useful for determining gene expression profiles in specific cells, for modulating gene expression in specific cells, and for making genetically modified eukaryotes. The present sequence represents an exemplary histone deacetylase chromatin-associated protein complex
                           ABG72115 standard;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 411 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes chimeric histone acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 61; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New chimeric polypeptide comprising a histone acetyltransferase polypeptide segment and a segment comprising a histone deacetylase chromatin-associated protein complex subunit, useful for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-175280/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histone acetyltransferase; histone deacetylase; chromatin-associated protein; gene expression.
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamuro J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     which can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDADQRIIKQLEYYFGNI
                                                                                                                                                             DELNOKI IRQVEYYFSD
                                                                                                                                                                                                            DDADQRIIKQLEYYFGN 17
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                        peptide;
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                                                                                                                                                                                                                                                                                          60.0%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       used
                                                                                                                                                                                                                                                                                                                                                                                                                                                  to produce chimeric polypeptides of
                              18
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                                                                                                                                                                                                                                                                                          Score 57;
Pred. No.
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Pred. No. 5e-09;
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                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                            DB 6;
0.53;
                                                                                                                                                                                                                                                                                                                     Length 411;
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RESULT 4
ANG47714
ID ANG47714
XX ANG47714
AC ANG4
AC ANG4
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal ribosome viral life cycle;
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                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                               AAG47714 standard; protein; 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compound containing acidic and aromatic amino acids, antiviral therapy in pharmaceutical, veterinary or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dasgupta
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                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                           18-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agricultural/horticultural applications.
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horticultural; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ģ
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entry site initiated translation; La antigen protein;
antiviral therapy; pharmaceutical; veterinary;
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56.2%;
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Pred. No. 0.03;
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promoter;
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06-SEP-2000.

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                      Scoring table:
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seq length: 2000000000
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95
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1: geneseqp1980s:*
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Maximum Match
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqp2000s:*
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score greater t
and is derived is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

25	24	23			20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	IJ	4	w	N	۳.	Result No.
45	45	45	45	45	45	45	46	46	47	47	48	48	48	48	48	48	50	50	54	54	54	. 55	57	95	Score
47.4	47.4	47.4	47.4	47.4	47.4	47.4	48.4	8	49.5	9.	0	٥.	50.5	0		0	ν.		56.8	٠,	٠,	57.9	60.0	100.0	Query Match
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ABB58137	ADB10474	ADB10476	ABB80984	AAM25632	ABP77967	ABG72102	ABM72091	ABJ19009	AAE34638	AAY64613	ABG01240	AAG91310	AAB95622	AAW00081	AAY92337	AAB93709	ABB65316	ABG72119	AAG47712	AAG47713	AAG47714	ABG72115	ABP70526	ABG72117	ID
Abb58137 Drosophii		Adb10476 Alloiococ	Abb80984 Murine A2	Aam25632 Human pro	Abp77967 N. gonorr			_				C glut		Aaw00081 Human int	Aay92337 Human Ini		Abb65316 Drosophil							Abg72117 Viral rep	Description

4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	20
44	44	44.5	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	4
46.3	46.3	46.8	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4	47.4		
18	17	823	1145	1145	1145	1145	1145	1145	1145	1115	1115	1109	1109	1082	1082	1076	1076	1062	7007
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AAY52200	ABG72113	AAW98507	ABO19416	ABO19417	ABG95849	ABG95848	AAB62247	AAU01023	AAY92322	AAB62249	AAU01025	AAB62240	AAU01016	AAB62239	AAU01015	ABO19418	ABG95850	AAB62238	PHOUTOTH
Aay52200	Abg72113	Aaw98507	Abo19416	Abo19417	Abg95849	Abg95848	Aab62247	Aau01023	Aay92322	Aab62249	Aau01025	Aab62240	Aau01016	Aab62239	Aau01015	Abo19418	Abg95850	Aab62238	DOCUMENT
Human	Viral	H. pyl	Human	Human 1	_	_	Human	Human	Human	Human	Human	Training.							
La	rep	lori	cal	cal	cal	rec	cal	Sec	аlр	cal	T TM	cal	Sec	cal	Sec	cal	cal	Cal	

ALIGNMENTS

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RESULT 1
ABG72117
Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide.
                                                                                                                                                                                           24-OCT-2002.
                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                   Viral replication inhibiting peptide, C. ELEGANS
                                                                                                                                                                                                                                                                                 28-JAN-2003
                                                                                                                                                                                                                                                                                               ABG72117;
                                                                                                                                                                                                                                                                                                            ABG72117 standard; peptide;
                                                                                                                                                                                                        WO200283858-A2
                                                                                                                                                                                                                                                                                 (first entry)
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12-APR-2002; 2002WO-US011589.

16-APR-2001; 2001US-00836073.

(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

Dasgupta A, Das S, Baidya N;

WPI; 2003-058634/05.

New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.

Claim 1; Page 15; 19pp; English.

The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La untigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 18 AA;

This Poloe Blonk (USO/O)

Search completed: September 10, 2004, 18:11:56 Job time : 42.6642 secs

Page 5

FILE REFERENCE: 220002054822

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GENERAL INFORMATION:

APPLICANT: Dasgupta, Asim

APPLICANT: Dasy, S.

APPLICANT: Baidya, Narayan

ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION

FILE REFERENCE: 220002054822

CURRENT APPLICATION NUMBER: US/09/836,073

CURRENT FILING DATE: 2002-10-24

PRIOR APPLICATION NUMBER: 09/316,630

PRIOR FILING DATE: 1999-05-21

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 18

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-836-073-10
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US-09-836-073-2
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US-09-836-073-10
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US-09-836-073-12
                                                                                             GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 1902-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PASTSEQ for Windows Version 4.0 SEQ ID NO 12
                                                           NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09836073 Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09836073 Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 17; Conserv
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Best Local Similarity 89.5%;
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
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TYPE: PRT
                        LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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89.5%;
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Pred. No. le
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Pred. No. 1.5e-05;
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GENERAL INFORMATION:

APPLICANT: Dasgupta, Asim
APPLICANT: Dasg. S.
APPLICANT: Dasidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION UMBER: 09/316,630
PRIOR APPLICATION UMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF Sep ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4
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US-09-836-073-4
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US-09-836-073-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                            Matches
                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                          APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Bais, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS: TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEC IN NGS: 99-05-21
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EAKICHQI-EYYFGDF 18
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78.9%;
                                                                                          73.6%;
93.8%;
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84.2%;
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                                                                                          Score 76.5; DB 9;
Pred. No. 4.4e-05;
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Pred. No. 4.4e-05;
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Pred. No. 4.4e-05;
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Matches

Conservative

0; Mismatches Score 88.5; Pred. No. 1.

.7e-05; DB 14;

Indels Length

Gaps

460;

Query Match Best Local Similarity

85.1%; 94.7%;

US-10-102-806-695

TYPE: PRT ORGANISM: Homo sapiens

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RESULT 7 US-10-264-049-2643

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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Birse et al.
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA139P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 2643
LENGTH: 460
                                                                                                                                           ; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13
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US-10-264-049-2643
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                                                        Query Match
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dasgupta, Asim APPLICANT: Das, S. APPLICANT: Baidya, Naraya
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                                  N
                                ALEAKICHQIEEYYFGDF 19
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94.7%;
                                                                                       81.2%;
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                                                                                        Score 84.5;
Pred. No. 2.
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Pred. No. 1.7e-05;
                                                                       Mismatches
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                                                                                          2.3e-06;
                                                                                                         DB 9;
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                                                                                                         Length 17;
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RESULT 9
US-09-836-073-11
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US-09-836-073-9
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                                                                                                                                                      RESULT 11
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APPLICANT: Dasgupta, Asim
APPLICANT: Dassys,
APPLICANT: Dassys,
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054825;
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
                                                                       Sequence 12, Application UPatent No. US20020173475A1
GENSRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo Sapiens
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nes 17; Conservative
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al Similarity 89.5%;
17; Conservation
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                                                                                                               Application US/09836073
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94.4%;
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Pred. No. 5e-06;
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Pred. No. 3
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TO INHIBIT VIRAL REPLICATION

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US-09-836-073-14
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1
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Best Local Similarity 94.7
18; Conservative
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SOFTWARE: PRSTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 18
TYPE: PRT
ORGANISM: Bovine
S-09-836-073-14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: WETHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
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TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                  TITLE OF INVENTION: ANALYSIS METHOD FILE REFERENCE: 532682000100
                                                     APPLICANT:
                                                                                       APPLICANT:
                                                                                                                                                                                         APPLICANT: Ward, Neil Raymond APPLICANT: Mundy, Christopher
CURRENT APPLICATION NUMBER: US/10/170,385
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                                                                                   Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                     Harris, Robert Alan
White, Jonathan
                                                                  Kingsman, Susan Mary
                                                                                                                                                                                                                                                Application US/10170385 o. US20030203372A1
                                                   Krige, David
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                                                                                                                                                                                             Christopher Robert
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94.7%;
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Pred. No. 5.
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.7e-07;
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US-10-102-806-695
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; ORGANISM: Homo sapiens
US-09-925-298-695
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US-09-925-298-695
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US-10-170-385-477
                                                     CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 695
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NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 477
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
LENGTH: 460
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                               Sequence 695, Application US/10102806 Publication No. US20030054421A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 695, Application US/09925298 Publication No. US20020039764A1
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Best Local Similarity 94.7%;
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PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
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TYPE: PRT
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94.7%;
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Pred. No. 1.
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Scoring table:
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
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143.151 Million cell updates/sec
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104
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 16, Appli Sequence 1, Appli Sequence 477, App Sequence 477, App Sequence 695, App Sequence 695, App Sequence 2643, App Sequence 13, Appl Sequence 13, Appl Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli	Description

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43.8	43.8	43.8	43.8	43.8	43.8	44.7	45.2	45.2	46.6	46.6	46.6	46.6	46.6	46.6	46.6	47.1	55.3	55.8	55.8	55.8	55.8	55.8	55.8	60.1	60.6	62.0	63.0	70.7	72.6
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109	Sequence 92, Appl	Sequence 95, Appl	Sequence 18, Appl	Sequence 60, Appi	Sequence 1146, Ap	Sequence 19, Appi	Sequence 5, Appli	Sequence 6, Appil	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 215, App	25	Sequence 25, Appl	25,	Sequence 5455, Ap	Sequence 214, App	Sequence 24, Appl	Sequence 20, Appl			_		8					

ALIGNMENTS

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US-09-836-073-16

(Sequence 16, Application US/09836073

(Sequence 16, Application US/09836073

(Sequence 16, Application US/09836073

(Sequence 10, Application US/09836073

(ENERAL INFORMATION:

(APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Narayan
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
(FILE REFERENCE: 220002054822

(CURRENT APPLICATION UNMBER: 09/09/336,073

(CURRENT FILING DATE: 2002-10-24

(PRIOR APPLICATION UNMBER: 09/316,630

(PRIOR APPLICATION UNMBER: 09/316,630

(PRIOR PILING DATE: 199-05-21

(NUMBER OF SEQ ID NOS: 19

(SEQ ID NO 16

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(SEQ ID NOS: 19

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Q7Z7P4;
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Q1-QCT-2003 (TrEMBLrel. 25, Last seque
Q1-QCT-2003 (TrEMBLrel. 25, Last annot
Similar to RIEN CDNA 1200017A24 gene
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01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein AF1134,
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TISSUE-Spleen;
MEDLINE-22388257; PubMed-12477932;
Strausberg R.L., Feingold E.A., Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reducing archaeon Archaeoglobus Nature 390:364-370(1997).
EMBL; AE001026; AAB90123.1; -.
                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                 SEQUENCE
                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                      Homo sapiens (Human)
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CA Dailide G., Ogura M., Dailide G., Golosely related, and distinct from the general from the communication of the EMBL/GenBank/DDBJ databases DR GO: 0018815; P. AAN74490.1; T. CO: 00008881; F: glutamate racemase activity; IEA. DR GO: 00008881; P. metabolism; IEA. T. GO: 00009252; P. peptidoglycan biosynthesis; IEA. T. GO: 0009252; P. peptidoglycan biosynthesis; IEA. T. GO: 0009252; P. peptidoglycan biosynthesis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Generation and initial analysis of more than 15,000
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BR 1 1
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   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dailidiene D., Berg D.E.;
in Helicobacter pylori: Gene pools of Spain and
ed, and distinct from those of Japan.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epsilonproteobacteria; Campylobacterales;
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   Score 45;
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01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein orf357
ORF357.
                           PIR;
                                                            Douglas S., Zauner S., Fraunholz M., Beaton M., Wu X., Reith M., Cavalier-Smith T., Maier U.G.; "The highly reduced genome of an enslaved algal Nature 410:1091-1096 (2001).
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01-OCT-2001
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ProDom; PD001819; PSI_RLU; 1.
TIGRFAMs; TIGR00005; rluD_subfam;
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GO; GO:0004730; F:pseudouridylate synthase activity;
GO; GO:0003733; F:NNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoshino C., Ishikawa J., Yamashita A., Valleri M., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M., "The complete genomic sequence of Mycoplasma penetrans, intracellular bacterial pathogen in humans."; hincaceliular bacterial pathogen in humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22354719; PubMed=12466555;
Sasaki Y., Ishikawa J., Yamashita
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01-MAR-2003
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                                                                                                                                                                                                                                        Guillardia theta (Cryptomonas phi).
Eukaryota; Cryptophyta; Cryptomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                   Q98SC2
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                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21223349; PubMed=11323671;
                                                                                                                                                                                                             EUKATYOTA; CTYPTOPHYTA;
NCBI_TaxID=55529;
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InterPro; IPR006225; Pseud synth Rlub.
InterPro; IPR006224; Rlu synth.
InterPro; IPR002942; S4.
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                        ; AF083031; AAK39661.1; -. H90120; H90120.
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    IPR001680; WD40
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Pred. No.
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                                                                                                                                Penny S.,
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Q04639;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-OCT-2002 (TrEMBLrel. 22, L
Chromosome XIII COSMID 9745.
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01-JUN-1998
01-JUN-2003
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Hypothetical protein;
SEQUENCE 357 AA; 42
                                                                   Barrell B., Rajandream M.A.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ
EMBL; Z38114; CAA86253 1.
                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M., Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. EMBL, ALOZZ117; CAA17931.1; -- PIR; T39314; T39314; T39314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomyceteses; Schizosaccharomycetaceae;
                                               EMBL; Z38114;
SEQUENCE 28
                                                                                                                                                                                               STRAIN=AB972;

Bowman S., Churcher C.;

Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 448 AA; 51190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SPBC119.16C.
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                                                                                                                                  SEQUENCE FROM N.A. STRAIN=AB972;
                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GeneDB_SPombe; SPBC119.16c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=972h-;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
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9; Conser
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nilarity 47.4%;
Conservative
                                                 284 AA;
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n; Repeat; WD repeat.
42401 MW; 71AEB9F896A04C82 CRC64;
                                                 32882 MW;
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ota; Schizosaccharomycetes;
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Last annotation updat
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      Score
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                                                 200EEB06A92A3CCF CRC64;
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      Length 284;
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Best Local S
Matches 8
                                                                                                                                                                         PRINTS;
SMART; S
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01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to sjogren syndrome antigen B (Autoantigen La).
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
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Bacteria; Aquificae;
NCBI_TaxID=63363;
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01-JUN-2003
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01-AUG-1998
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                                                                                                                                                                                                                                                                                                        Submitted (JAN-2003) to the EMBL/GenBank/DDBJ EMBL; BC045392; AAH45392.1; -. GO; GO:0005634; C:nucleus; IEA. GO; GO:0003723; F:RNA binding; IEA. InterPro; IPR002344; Lupus La. InterPro; IPR006630; Lupus La. InterPro; IPR006630; RNA_rec_mot.
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EMBL; AE000757; AAC07635.1;
PIR; B70456; B70456.
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                                                      PROSITE; PS00030; RRM; 1.

PROSITE; PS00030; RRM_RNP_1; 1.

SEQUENCE 401 AA; 46138 MW;
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                                                                                                                                                                                                                                                                              Pfam; PF00076; rrm; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                      ; PR00302; LUPUSLA.
SM00715; LA; 1.
SM00360; RRM; 1.
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8; Conserv
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72.7%;
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   49.5%;
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24,
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Pred. No. 0.31;
   Score 51.5;
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Query Match

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01-OCT-2002 (TremBLrel. 22, La.
01-JUN-2003 (TremBLrel. 24, La.
Hypothetical protein Cgl1775.
CGL1775.
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Q8YZF2;
01-MAR-2002
01-MAR-2002
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Q8NPN6;
01-OCT-2002
                                                                                                                                                            MEDLINB-21595285; FUDDWEUGLAGO CO., KURITZ T., S
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., S
Watanabe A., Iriguchi M., Ishikawa A., Kawashim
Kishida Y., Kohara M., Matsumoto M., Matsuno A.
Nakazaki N., Shimpo S., Sugimoto M., Takazawa N
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous I
                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (bu...
Anabaena sp. (bu...
Anabaena; Cyanobacteria;
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PROSITE; PS00433; FKBP PPTASE 1; 1.

Hypothetical protein; Complete proteome.
SEQUENCE 2169 AA; 240194 MW; 4AEB029
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STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDILINE=21595285; PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of Corynebacterium submitted (MAY-2002) to the EMBL/GenBank/DDBJ
                                                          EMBL, AP003582; BAB72466.1; -. PIR; AC1870; AC1870; Hypothetical protein; Complete SEQUENCE 187 AA; 21553 MW;
                                                                                                                   cyanobacterium Anabaena sp. DNA Res. 8:205-213(2001). EMBL; AP003582; BAB72466.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical ALR0508.
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Nostocales; Nostocaceae;
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M., Matsuno A., N
M., Takazawa M.,
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No.
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A., Kawashima K., Ki
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Best Local S
Matches 17
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STRAIN=NOD; TISSUE=Thymus;

STRAIN=NOD; TISSUE=Thymus;

STRAIN=NOD; TISSUE=Thymus;

MEDLINE=22354683; PubMed=12466851;

The FANTOM Consortium,

I wanalysis of the mouse transcriptome based on functional ann

I 60,770 full-length cDNAs.";

Nature 420:563-573(2002).

R ANGUE 420:563-573(2002).

R EMBL, AKO88677; BAC40498.1; -.

R MGD; MGI:98423; Sab.

R GO; GO:0005634; C:nucleus; IDA.

R InterPro; IPR006630; Lupus La_dom.

InterPro; IPR006630; Lupus La_dom.

InterPro; IPR006630; RNA_rec_mot.
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 Q7ZTK2
Q7ZTK2;
01-JUN-2003
01-JUN-2003
01-OCT-2003
Similar to 1
                                                                                                                                                                                                                                   PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PSS0102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
SEQUENCE 415 AA; 47657 MW; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pfam; PF00076; rrm; 1.
PRINTS; PR0030C2; LUPUSLA.
SMART; SM00715; LA; 1.
SEQUENCE 381 AA; 43891 MW;
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InterPro; IPR002344; Lupus_La.
InterPro; IPR00630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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Pfam; PF00076; rrm; 1
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01-MAR-2003
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RESULT 4
BQCHIS
ID 080H
AC 080H
AC 080H
DT 01-J
DT 01-J
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DE Untr
GN UBP:
OS Gall:
OC Enka
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OX NCBI
RN [1]
RP SEQU
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Matches 12
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Best Local
                                                 Matches
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Submitted (FEB-2003) to the EMBL/GenE
Submitted AAH46654.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La.
InterPro; IPR006630; Lupus La.
InterPro; IPR000504; RNA_rec_mot.
Pfem; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                          L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMBL/GenE
EMBL; AR467897; AAL76269.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR002344; Lupus La dom.
InterPro; IPR000504; RNA_rec_mot.
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OLJUN-2002 (Trembirel. 21, Created)

OLJUN-2002 (Trembirel. 21, Last sequence update)

OLJUN-2002 (Trembirel. 25, Last annotation updat

Thranslated region binding-protein.
                                                                                                                                                                                                                     Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
'SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRW; 1.
SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;
                                                                                                                                               PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; SEQUENCE 206 AA; 23992 MW;
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Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
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                                              l Similarity
12; Conserv
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LEAKICHQIEEYYFGD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
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                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                      56.2%;
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75.0%;
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Pred. No. 0.19
1; Mismatches
                                                                                                                                                                         -
                                                                        Score 58.5;
Pred. No. 0.
                                                                                                                                                    965B62F7DFFB90E9 CRC64;
                                                    Mismatches
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0.19;
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LESKICQQI-EYYFGN

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Sequence:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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        September 10, 2004, 17:29:01; Search time 43.5196 Seconds (without alignments)
137.751 Million cell updates/sec
                                                                                                                                                                                         SPTREMBL 25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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104
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sp_human.*
sp_invertebrate:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_mhage:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*
sp_unclassified:*
sp_bacteriap:*
sp_archeap:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	1 L	13	12	11	10	9	89	7	σ.	ហ	4	ω	2	ם	Result No.
45	4 5 4 5 5	46	46	47	47	47	47	49	51.5	55	58.5	59.5	84.5	84.5	Score
43.3	44.8	44.2	44.2	45.2	45.2	45.2	45.2	47.1	49.5	52.9	56.2	57.2	81.2	81.2	Query Match Length DB
184	166	456	284	448	357	301	187	2169	401	135	206	427	415	381	ngth
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Q7X5D8	086802	029131	Q04639	042907	Q98SC2	Q8EX37	Q8YZF2	Q8NPN6	Q7ZTI0	067676	Q8QHI5	Q7ZTK2	Q8BTU4	дэсүвэ	ij
	O8gk02 helicobacte	-	Q04639 saccharomyc	O42907 schizosacch	Q98sc2 guillardia	Q8ex37 mycoplasma	Q8yzf2 anabaena sp	Q8npn6 corynebacte	Q7zti0 brachydanio	067676 aquifex aeo	08qhi5 gallus gall		Q8btu4 mus musculu	Q9cyb9 mus musculu	Description

45	44	43	42	41	40	39	38	37	36 6	კ 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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41.3	41.3	41.3	41.3		41.3				42.3	42.3	42.3	42.3	42.3	42.3	42.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3	43.3		43.3	43.3	43.3	43.3
510	447	427	427	297	185	119	888	658	627	627	627	592	505	284	281	1676	1164	1164	1164	1164	1164	1164	1164	1156	928	748	409	231
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Q43819	Q93V61	Q7TWY2	005874	Q9H1U9	Q9UAF3	Q9ZP89	Q873B9	Q86BB2	Q7YUZ6	Q86MC2	Q8IEX1	Q9VN01	Q85V94	Q8NG50	Q9CQK3	Q85FR6	Q80DV1	Q8V2N1	Q8V4V3	Q8JL90	Q90031	Q9JF79	Q90027	057230	Q9LJ02	Q8AAX3	Q98RP4	Q7X5E0
Q43819 pisum sativ	arabi			3	Q9uaf3 polyandroca	Q9zp89 neurotheca	Q873b9 neurospora		Q7yuz6 trypanosoma	Q86mc2 trypanosoma	Q81ex1 trypanosoma				3 mus	cyani	-			Q8j190 ectromelia		vaccini			Q91j02 oryza sativ	ω	ш	

ALIGNMENTS

pgcymb9 preliminary; prt; 381 AA. AC OSCYB9; DT 01-UN-2001 (TrEMBLrel. 17, Created) DT 01-UN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-UN-2001 (TrEMBLrel. 17, Last sequence update) DT 01-CT-2003 (TrEMBLrel. 17, Last sequence update) DT 01-CT-2003 (TrEMBLrel. 25, Last annotation update) DT 01-CT-2003 (TrEMBLrel. 25, Last annotation update) DT 01-CT-2003 (TrEMBLrel. 25, Last annotation update) DS SB. GN Mus musculus (Mouse). CN Mus Mus musculus (Mouse). CN Mus Musculus (Mus Musculus (Mus Musculus (Mus Musculus (Mus Musculus (Musculus (Musculus (Muscu
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Search completed: September 10, 2004, 17:53:09 Job time: 9.64246 secs
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                                                                                                                                              Query Match 43.3%; Score 45; DB 1; Length 1164; Best Local Similarity 56.2%; Pred. No. 22; Matches 9; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                  Pfam; PF00562; RNA pol Rpb2_6; 1.
Pfam; PF04560; RNA pol Rpb2_7; 1.
PROSITE; PS01166; RNA POL BETA; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Zinc-finger.
ZN FING 1087 1106 C4-TYPE (POTENTIAL).
SEQUENCE 1164 AA; 133329 MW; 0452B84ED810CD53 CRC64;
                                                                        505 LEKKICEYIRSYYKDD 520
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RESULT 14
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ZN FING
SEQUENCE
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation updat
16-OCT-2001 (Rel. 40, Last annotation updat
        EMBL; M35027; AAA48148.1; -. PIR; H42519; RNVZ8T.
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE STRAIN-Copenhagen;
STRAIN-Copenhagen;
MEDLINE-91021027; PubMed-2219722;
MEDLINE-91021027; PubMed-2219722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen). Viruses; deBNA viruses, no RNA stag Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-directed RNA polymerase 132 kDa RPO132 OR A24R.
                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                           STRAIN=Copenhagen;
Goebel S.J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification, sequence, second-largest subunit of boolymerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91082452; PubMed=1824607; Amegadzie B.Y., Holmes M.H., Cole N.B.,
                                                                                                                                                                     -!- SUBUNIT: This enzyme consists of at least eight subunits.
-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                 Paoletti E.;
                                                                                                                                                                                                                                                                                                                                        COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                 "The complete DNA sequence of vaccinia virus.";
Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                             Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10254, 10249;
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                                                                                                                                                                                       \{RNA\}(N). SUBUNIT: This enzyme consists of at least
                                                                                                                                                                                                                  substrates.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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                                        M37415; AAA72882.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180:88-98(1991).
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1106
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RNA_pol_B
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Pred. No.
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                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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22;
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RESULT 15
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InterPro; IPR007646; RNA pol Rpb2_4.
InterPro; IPR007647; RNA pol Rpb2_5.
InterPro; IPR007647; RNA pol Rpb2_6.
InterPro; IPR007120; RNA pol Rpb2_7.
Pfam; PF04565; RNA pol Rpb2_3; 1.
Pfam; PF04565; RNA pol Rpb2_4; 1.
Pfam; PF04567; RNA pol Rpb2_5; 1.
Pfam; PF04567; RNA pol Rpb2_6; 1.
Pfam; PF04567; RNA pol Rpb2_7; 1.
Pfam; PF04560; RNA pol Rpb2_7; 1.
Pfam; PF04560; RNA pol Rpb2_7; 1.
PROSITE; PS01166; RNA POL Rpb2_7; 1.
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P33811;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restitute by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAINSINGLA-1967 / Isolate Ind3;

MEDLINE=93202281; PubMed=8384129;

Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;

"Genes of variola and vaccinia viruses necessary to overcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation updat
01-FEB-1996 (RNA polymerase 132 kDa polypep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variola virus.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphat (RNA) (N).
SUBUNIT: This enzyme consists of at least eight subunits.
SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   substrates.
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1164 AA; 133363 MW; B1F5C1484BA37D0
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MBL outstation -
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16-OCT-2001
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Submitted (MAY11996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYN
IT CAN HYDROLYZE BUTYRYLTHIOCHOLINE.
-i- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acet
-i- SUBUNIT: Oligomer composed of disulfide-linked homodimers
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   SEQUENCE
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InterPro; IPR000997; Cholinesterase.
InterPro; IPR000379; Ser_estrs.
Pfam; PF00135; COesterase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X75331; CAA53080.1; -.
EMBL; U58731; AAB00593.1; -.
PIR; A54413; A54413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
MEDLINE=94193691; PubMed=8144590;
Arpagaus M., Fedon Y., Cousin X.,
Fournier D., Toutant J.-P.;
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Acetylcholinesterase 1 precursor (EC 3.1.1.7)
                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase;
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WormPep; W09B12.1; CE07569.
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                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00878; CHOLNESTRASE.
                                                                                                                                                                                                                                                                                                                                                                                                               Neurotransmitter
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A NON-CATALYTIC SUBUNIT.
DEVELOPMENTAL STAGE: DETEC
ABUNDANT IN LARVAL STAGES
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                                                                                                                                                                                                                                                                                                                                                                                                  PS00122; CARBOXYLESTERASE B 1; 1.
PS00941; CARBOXYLESTERASE B 2; 1.
pS00941; CARBOXYLESTERASE B 1; 1.
pS00941; CARBOXYLESTERASE B 2; 1.
pS0094
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(Rel. 30,
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Last sequence update)
Last annotation updat
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                  ACETYLCHOLINESTERASE 1.
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N IN EMBRYOS OR
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Best Local S
Matches
                                                                                              InterPro; | IRR007121; RNA DOL B.
InterPro; | IRR007645; RNA DOL Rpb2 3.
InterPro; | IPR007645; RNA DOL Rpb2 4.
InterPro; | IPR007647; RNA DOL Rpb2 5.
InterPro; | IPR007647; RNA DOL Rpb2 7.
InterPro; | IPR007120; RNA DOL Rpb2 7.
InterPro; | IPR007120; RNA DOL Rpb2 7.
InterPro; | IPR007120; RNA DOL Rpb2 7.
InterPro; | IPR007641; RNA DOL Rpb2 7.
InterPro; | IPR00766; RNA DOL Rpb2 7.
InterPro; | IPR007646; RNA DOL Rpb2 7.
InterPro; | IPR00764; RNA DOL Rpb2 7.
InterPro
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01-AUG-1990 (Rel. 15, Created)

01-AUG-1990 (Rel. 15, Last sequence update)

01-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                EMBL; M26173; AAA42919.1; -.
EMBL; M26173; AAA42920.1; -.
PIR; A31879; RNVZCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Brighton red;
MEDLINE=89125698; PubMed=2915377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patel D.D., Pickup D.J.,
Patel D.D., Pickup D.J.,
"The second-largest subunit of the poxvirus RNA polymerase is some second-largest subunits of procaryotic and eucaryotic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cowpox virus (CPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: This enzyme consists of ALTERNATIVE PRODUCTS: Event=Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: DNA-dependent of DNA into RNA using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the RNA polymerase beta chain family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COWPX
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                                                            DNA-directed RNA polymerase, Alternative initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.3%;
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  POLYPEPTIDE,
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                                          DNA-DIRECTED
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                        RNA POLYMERASE ISOFORM 1.
                                                                                     Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Ray J., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human Par and mouse CDMA."
                                                                                                                     Matches
                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones."; DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins activate some small GTPases by exchanging bound GDP free GTP (By similarity).
-!- TISSUE SPECIFICITY: Widely expressed. Expressed at low level spleen, cerebellum, hippocampus and in substantia nigra.
-!- DOMAIN: The DHR-2 domain may mediate some GEF activity (By
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                              Guanine-nucleotide releasing factor. DOMAIN 548 786 DHR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cote J.-F., Vuori
                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
SIMILARITY: Belongs to the DOCK family.
SIMILARITY: Contains 1 DHR-1 (CZH-1) domain.
SIMILARITY: Contains 1 DHR-2 (CZH-2) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse
1780
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                                                       ຫ
                                                                                                                     Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S
an email to license@isb-sib.ch).
                                                          AKICHQIEEYY---FGD
                                                                                                                                                                                                                                                                                                                                                                            IPR002016;
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                                                                                                                        Conservative
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AAH08335.1; -.
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                                                                                                                                                                                                                                                                                 2012
                                                                                                                                                     43.8%;
                                                                                                                                                                                                                                                                                                                                                                            Peroxidase.
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                                                                                                                        4.
                                                                                                                                                     Score 45.5;
Pred. No. 3
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RESULT 11 ACE1_CAEBR

STANDARD;

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RESULT 12
ACE1_CAEEL
ID ACE1_CAEEL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of class A, in the two nematodes Caenorhabditis Caenorhabditis briggsae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Hydrolase; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;
Neurotransmitter degradation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00878; CHOLNESTRASE.
PROSITE; PS00122; CARBOXYLESTERASE_B_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A NON-CATALYTIC SUBUNIT (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grauso M., Culetto E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97069944; PubMed=8912924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis briggsae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                    Similarity
8; Conserv
                                                                                                         CIQSEDTYFGDF
                                                                                                                                CHQIEEYYFGDF 19
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IPR000379; Ser_estrs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Berge J.B., Toutant J.-P., Arpagaus M.; of ACE-1, the gene encoding acetylcholinesterase
                                                                                                         93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oda; Chromadorea; Rhabditida; Rhabditoidea; Caenorhabditis.
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OF COLUMN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTELLINKED (GLCNAC. . .)) (POTELLINKED (GLCNAC. . .) (POTELLINKED (GLCNAC. . .)) (POTELLINKED (GLCNAC. .
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Pred. No.
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11;
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RESULT 9
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       Seees
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Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanagin A., Matsuda H., Batalov S., Beisel K.W.,

Schriml L.M., Kanagin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Garidt D., Hitcher C.F., Forrest A., Frazer K.S.,

Cassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Gassterland T., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Na Kanajott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Na Naglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Na Nagashina T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petroveky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Na Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
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Best Local :
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TRANSMEM
TRANSMEM 2
TRANSMEM 3
SEQUENCE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain, and
STRAIN=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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10-OCT-2003 (Re
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                                                                                                                                                                                                                                                  SEQUENCE OF 640-849 FROM N.A. STRAIN=C57BL/6J; TISSUE=Testis;
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10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                     MEDLINE=22354683; PubMed=12466851;
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9; Conserv
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352 AA;
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24 44 POTENTI
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332
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Rodentia;
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Last annotation update)
ssis protein 6 (Fragment)
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Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast tumor;
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, Gojobori T.,
h J.,
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RESULT 10
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Best Local S
Matches 9
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096HPD, 0992F2;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

15-MAR-2004 (Rel. 43, Dast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yanaki R., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
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DOC6_HUMAN
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Nature 420:563-573(2002).
-!- FUNCTION: Potential guar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers
Birney E., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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EMBL; BC043042; AAH43042.1;
EMBL; AK016777; BAB30423.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a convergent the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                            TISSUE=Brain;
MEDLINE=22158633;
                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guanine-nucleotide releasing
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                                                                                                      REVISIONS
                                                                                                                                                                                                                                                                                                    Nagase T.,
                                                                                                                                                                                                                                                                                                                                    MEDLINE=20181126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                        Prediction of the
                                                                                                                                      complete sequences of 150 new cDI large proteins in vitro.";
Res. 7:65-73(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Potential quanine nucleotide (
FUNCTION: Potential guanine small GTPases by
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DOMAIN: The DHR-2 domain may mediate some GEF activity (By
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849 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
8633; PubMed=12168954;
Okazaki N., Yamakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            profit institutions as long as its content
                                                                                                                                                                                                                                                                                                 PubMed=10718198;
R., Ishikawa K.-I.,
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   Yamakawa H.,
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PROSITE; PS00030; RRM RNP_1; 1.
PRNA-binding; Nuclear protein; P
DOMAIN 111 203 RN
                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schumann R.R., Leong S.R., Flaggs G.W., Gray I Mathison J.C., Tobias P.S., Ulevitch R.J.; "Structure and function of lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86306528; PubMed=2427635;
Tobias P.S., Soldau K., Ulevitch R.J.;
"Isolation of a lipopolysaccharide-binding acute phase reactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                               rabbit serum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
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                                                                                                                                                                                                         EXp. Med. 164:777-793(1986).

FUNCTION: Binds to the lipid a moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in membrane of all Gram-negative bacteria. The LBP/LP to interact with the CDL1 receptor.
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L-NOV-1990 (Rel. 16, Last sequence upl-OCT-2003 (Rel. 42, Last annotation propopolysaccharide-binding protein pro
ween the Swiss Institute of Bioinformate Buropean Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed ities requires a license agreement (See
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Pfam; PF02886; LBP BPI CETP_C; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288c / AB972;
STRAIN-S288c / AB972;
MEDLINE-97313268; PubMed-9169872;
Bowman S., Churcher C.M., Badcock
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                                                                                                                                                 PIR; S48331; S48331
GermOnline; 142598;
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Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal
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                                                                                                                                                                                                                                                                       or send
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; S0004532; ERV41.
GG:0030138; C:COPII-coated vesicle; IDA.
GO:0030176; C:integral to endoplasmic reticulum
GO:0030173; C:integral to Golgi membrane; IDA.
GO:0006888; P:ER to Golgi transport; IPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane SIMILARITY: TO YEAST YALO42W AND S.POMBE
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                                                                                                                                                                                                             Z38114; CAA86254.1;
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Pred. No.
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N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
E-> G (IN REF. 2).
S-> F (IN REF. 2).
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Matches 17
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P28049;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last se
15-MAR-2004 (Rel. 43, Last an
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InterPro; IPR00630; Lupus_La dom.
InterPro; IPR006504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XENLA
                                                                                                                                                                                                                    expression.";
J. Mol. Biol. 231:196-204 (1993).
I. Mol. Biol. 231:196-204 (1993).
I. FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).

Polymerase III transcripts (By similarity).
I. SUBCELIULAR LOCATION: Nuclear (Probable).
I. DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly accumulate in stage III/IV occytes, then exhibit a roughly
  This SWI
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Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homolog
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PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; P
DOMAIN 111 187 RN
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                                                                       PTM: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of La, LaA and I
SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
SIMILARITY: Contains 1 RNA recognition motif (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          erly D., Stutz F., Lin-
proteins from Xenopus
                                                                                                                                                                                                      constant steady state level in mature
SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
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F., Lin-Marq N.,
Xenopus laevis. o
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Pred. No. 2.1e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA cloning and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; I
ia; Pipoidea;
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1.1e-06;
nes 0;
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through a cond the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
; Pipidae;
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                                                                                                                               LaB,
                                                                            domain.
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     a collaboration
MBL outstation -
                                                                                                                               in xenopus
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                              expression.";

J. Mol. Biol. 231:196-204(1993).

-i- FUNCTION: La protein plays a role in the tran polymerase III. It is most probably a transcr polymerase III. It is termini of virtually factor. Binds to the 3 termini of virtually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAA_XENLA
P28048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no recommend in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement (See http://www.isb-sib.ch/announce/
                                                                    This
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                                                                                                                                                                                                                                                                          <del>+</del> <del>+</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-MAR-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.

RNA-binding; Nuclear_protein; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scherly D., Stutz
"La proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
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                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93287095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homolog A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002344;
InterPro; IPR006630;
                                                                                                                                                                                                                          polymerase III transcripts (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly constant steady state level in mature oocytes, eggs, and earl-
                                                                                                                                PTM: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of La,
SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN
                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                  SIMILARITY: Contains 1 RNA recognition motif (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S33817;
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427 AA;
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Swiss Institute The Bioinformatics Institute. The Bioinformatics Institute as long
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l. 43, Last
n homolog A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8510143;
F., Lin-Marq N.,
Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Lupus_La_dom.; Lupus_La_dom.; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
annotation update)
(La ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59.5; I
Pred. No. 0.03
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA-BINDING (RRM).
NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45F3146F8934A355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Clarkson S.G.; cDNA cloning an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428
                                                                                                                                                                                                                                                                                                                                                                                       in the transcription of RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            developmental
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; Pipidae;
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                                                                                                                                                               LaB,
                                                                                                                  domain.
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Best Local :
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P38656;
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection of species-specific Gene 126:265-268(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Systemic lupus of Nuclear protein DOMAIN 111
                                                                                                          InterPro; IPR002344; Lupus_La.
InterPro; IPR00630; Lupus_La.dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP05383; La; 1.
Pfam; PF000076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSB OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
28-FEB-2003 (Rel. 41, Last ann
Lupus La protein homolog (La r
              PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
DOMAIN 111 187 RNA-BINDING (RRM)
                                                                  SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.M.
MEDLINE=93246255; PubMed=7916708;
MEDLINE=93246255; PubMed=7916708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                              PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                               PIR; JC1494; JC1494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation of rat cDNA clones coding for detection of species-specific variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bachmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a trually all nascent factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7.
                                                                                                                                                                                                                                                                                                                               PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                           X67859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS-B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00030; RRM_RNP_1; 1. lupus erythematosus; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366
408 AA;
  415 AA;
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                                                                                                                                                                                                                                                                                                                                                                        Interacts with DDX15
                                                                                                                                                                                            CAA48043.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
366
46837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l, Last sequence update)
  47777 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.1%;
94.7%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY CK2).
; EC153C15F9187FC4 CRC64;
               RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA-binding; Phosphorylation;
  033FD9CC1E475F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                         (By similarity)
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No. 4.
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1.5e-07;
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                                                                                                                                                                                                                                                                                           a collaboration -
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IA_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                RC STRAINSTEPMS/N. TISSUB-Mammary gland;

RX MEDLINE=22380257; PubMed=12477932;

RX MEDLINE=22380257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Jiatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Jiatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Joden T.B., Toshiyuki S., Carninci P., Prange C.,

RA Jrownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Stapleton M.J., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J.,

RA Rodrigues S., Sanchez R.M.,

RA Rodrigues S., Sanchez R.M.,

RA Rodrigues S., Sanchez R.M.,

RA Rodrigues 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LA MOUSE P32067;
                                                                                                                                                                           Groelz D., Bachmann M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor for
of RNA polymerase III transcripts including tRNA and 4.55, 55, ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Topfer F. Gordon T., McCluskey J.;

Topfer F. Gordon T., McCluskey J.;

"Characterization of the mouse autoantigen La (SS-B). Id

of conserved RNA-binding motifs, a putative ATP binding

of conserved RNA-binding motifs, a putative ATP binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSB OR SS-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993
01-OCT-1993
                                                                                     ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=93203630; PubMed=8454877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel.
01-OCT-1993 (Rel.
15-MAR-2004 (Rel.
                       This
                                                                                                                                                                                                                                                                                                                                                                                    Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoantibodies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homolog)
                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-11 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 150:3091-3100(1993).
                                                                                                     and 7-2 RNAs.
SUBGUNIT: Interacts with DDX15 (By similarity)
SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                   PTM: Phosphorylated (
SIMILARITY: Contains
  SWISS-PROT entry is copyright. een the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Natl. Acad. Sci. U.S.A. 99:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homolog (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27, Created)27, Last sequence update)43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.1%;
94.7%;
                                                                                       (By similarity)
                                                                   1 RNA recognition motif (RRM) domain
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                  99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; | Sciurognathi; Muridae;
  ght. It is produced through Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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.6e-07;
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; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoantigen
                                                                                                                                                                                    n precursor forms and 4.5S, 5S, 7S
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      EMBL outstation
                         a collaboration
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RESULT OF SERVICE CONTRACTOR SER
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                                                                                                                                                                                                                                  A Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Wall R., Wallyk S., Wall R., Wall 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chambers J.C., Kenan D., Martin B. "Genomic structure and amino acid autoantigen.";
J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P05455;
01-NOV-1988 (Rel. 09, Lieute appende upunce 01-UTL-1989 (Rel. 11, Last sequence upunce 15-MAR-2004 (Rel. 43, Last annotation update)
Lupus La protein (Sjogren syndrome type B antigen)
Lupus La protein) (La autoantigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
SEQUENCE
                                                                                                         Sturgess
Coppel R.
[<u>5</u>]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chan E.K.L., Sullivan K.F., Tan E.M., "Ribonucleoprotein SS-B/La belongs to sequences for RNA-binding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                             MEDLINE=88199081;
                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89202037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                   Characteristics
                            Immunol.
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                            140:3212-3218(1988)
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Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S Van Venrooij W.J., Pruijn G.J.M., Van der Heijden A., De Jong A.S "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, putative DEAH-box RNA helicase.";
RNA 8:1428-1443(2002).
                                                                                                                                 GO; GO:0030529; C:ribonucleoprotein complex; TAS
GO; GO:0003729; F:mRNA binding; TAS.
GO; GO:000049; F:tRNA binding; TAS.
GO; GO:0000334; P:histone mRNA metabolism; TAS.
GO; GO:0006400; P:tRNA modification; TAS.
                                                                                                                                                                                                                                        EMBL; J04205; AAA51885.1; -. EMBL; BC001289; AAH01289.1; -EMBL; BC020818; AAH20818.1; -- PIR; A31888; A31888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97207017; PubMed=9054510; Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Maraie R.J.; "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes."; [21] 88:707-715(1997)
              SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                          InterPro; IPR000504; Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                InterPro; IPR003344; Lupus La.
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                                             PRINTS;
                                                                                                                                                                                                                               Genew; HGNC:11316; SSB.
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                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Gottlieb E., Steitz J.A.;
"Function of the mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and 7-2 RNAs.
SUBUNIT: Interracts with DDX15.
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: PHOSPHORYLATED. THE PHOSPHORYLATION
C-TERMINAL PART OF THE PROTEIN.
PTM: The N-terminus is blocked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor for RNA polymerase III transcripts including tRNA and 4.58, 58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: Sera from patients with systemic lupus erythemato often contain antibodies that react with the normal cellul La protein as if this antigen was foreign.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                             PR00302;
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                                             LUPUSLA
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RNA polymerase
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Scoring table:
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Gapop 10.0 , Gapext 0.5
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104
1 AALEAKICHQIBEYYFGDF 19
SwissProt_42:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P50346 glycine max	ocean	1 homo	7	P40796 drosophila	7		P24177 escherichia		Ψ	Q9yas4 aeropyrum p	Q58458 methanococc	Q9h1u9 homo sapien	neisse	myzus	1 myzus	6 chlam		1 vario	vaccini	4.	P38433 caenorhabdi		0	Q8vdr9 mus musculu		P17454 oryctolagus	æ	P28049 xenopus lae	P32067 mus musculu	6 rattu	P05455 homo sapien	1 bos t	Description	•

ALIGNMENTS

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EMBL; X13698; CAA31986.1; PIR; S03849; S03849; Lupus_La. InterPro; IPR002344; Lupus_La_dom. InterPro; IPR005630; Lupus_La_dom. InterPro; IPR00504; RNA_rec_mot. Pfam; PF00383; La; 1. Pfam; PF00302; LUPUSLA. SMART; SM00302; LUPUSLA. SMART; SM00306; RRM; 1. PROSITE; PS50102; RRM; 1. PROSITE; PS50102; RRM_RNP_1; 1. PROSITE; PS00030; RRM_RNP_1; 1. PROSITE; PS00030; RRM_RNP_1; 1.	s SWISS-PROT entry is copyright. It is produced thr ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no by non-profit institutions as long as its contified and this statement is not removed. Usage by itles requires a license agreement (See http://www.send an email to license@isb-sib.ch).		SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=Pituitary; MEDLINE=89207037; PubMed=2468131; Chan E.K.L., Sullivan K.F., Tan E.M.; "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding."; Nucleic Acids Res. 17:2233-2244 (1989). -I- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.55, 55, 75, and 7-2 RNAs.	SSB. SSB. SSB. Bos taurus (Bovine). Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bummalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. NCBI_TaxID=9913;	BOVIN BOVIN STANDARD; PRT; 404 AA. P10881; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).

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A;Map position: X
A;Introns: 13/3; 59/2; 154/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2 C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase F;45-567/Domain: cholinesterase homology <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T37411

R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.

submitted to the EMBL Data Library, March 1997

A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain A;Reference number: Z20877

A;Accession: T37411
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A;Cross-references: EMBL:U58731; PIDN:AAB00593.1; GSPDB:GN00028
A;Experimental source: strain Bristol N2; clone W09B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase subunit rpo132 - vaccinia virus (strain Ankara)
C;Species: vaccinia virus
A;Variety: strain Ankara
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C;Date: 71-7011
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A;Gene: CESP:ace-1
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A; Accession: T29824
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C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1156 <ANT>
A;Cross-references: EMBL:U94848; PIDN:AAB96526.1
A;Experimental source: strain Ankara
Search completed: September 10, 2004, 18:02:35
Job time : 16.8603 secs
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                          Query Match 43.3%; Score 45; DB 2; Length 1156; Best Local Similarity 56.2%; Pred. No. 66; Matches 9; Conservative 0; Mismatches 7; Indels
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66.7%;
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lipopolysaccharide-binding protein - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_chang C;Accession: B35843; A46553 R;Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wrigh Science 249, 1429-1431, 1990 A;Title: Structure and function of lipopolysaccharide binding A;Reference number: A35843; MUID:90385281; PMID:2402637 A;Accession: B35843
hypothetical protein AF1134 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #tC;Accession: E69391
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C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
C;Accession: S48331; S48330
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A;Residues: 27-55,'XG',58-62,'F',64-65 <TOB>
C;Superfamily: lipopolysaccharide-binding protein
C;Keywords: acute phase
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C;Species: Saccharomyces cerevisiae
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A; Accession: A46553
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R;Tobias, P.S.; Soldau, K.; Ulevitch, R.J.
J. Exp. Med. 164, 777-793, 1986
A;Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit serva, Reference number: A46553; MUID:86306528; PMID:2427635
                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 13L
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A;Cross-references: SGD:S0004532
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A;Cross-references: EMBL
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A; Residues: 1-352 <BOW>
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A;Accession: S48331
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                                                                                                    RESULT 12
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;230-246/Domain: transmembrane #status predicted
;248-264/Domain: transmembrane #status predicted
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9; Conserv
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                 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
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56.2%;
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81.8%;
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Pred. No.
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirl Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, I Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P., Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reduc: A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: E69391

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                        R;Arpagaus, M.; Fedon, Y.; Cousin, X.; Chatonnet, A.; Berge, J.B.; Fournier, D.; Toutant J. Biol. Chem. 269, 9957-9965, 1994
A;Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene encod A;Reference number: A54413; MUID:94193691; PMID:8144590
A;Accession: A54413
R;Wu, X.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans co
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A;Genome: nucleomorph
C;Superfamily: translation releasing
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                                                                                   A;Molecule type: mRNA
A;Residues: 1-620 <ARP>
A;Cross-references: GB:X75331; NID:g475060; PIDN:CAA53080.1;
                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                          C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 21-Jul-2000
C;Accession: A54413; T29824
                                                                                                                                                                                                                                                                                                                                       acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans C_iSpecies: Caenorhabditis elegans
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A; Residues: 1-409 < DOU>
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R;Douglas, S.; Zauner, S.;
Rature 410, 1091-1096, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eukaryotic release factor 1 homolog [imported] - Guillardia theta nucleomorph C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
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Best Local
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G.; Gill, S.; Kirkness, E.F.
                                                                                     PID: g671831
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A;Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874 C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor.
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A; Residues: 1-428 < SCH>
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                                                                                                                                                                                                                                            C; Accession: AC1870
C; Accession: AC1870
R; Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, s.
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
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A;Experimental source: strain VF5
C;Genetics:
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AC1870
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Nature 392, 353-0-1
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70456
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: CNA
A;Molecule type: CNA
A;Residues: 1-187 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72466.1; PID:g17129853; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                         DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC1870
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein alr0508 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec
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A;Status: preliminar
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2; Mismatches
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09-Dec-2002
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RESULT B35843

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C; Species: nucleomorph Guillardia theta nucleomorph A; Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 C; Accession: H90120
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A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
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                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Moi scule type: DNA
A;Moi scule type: DNA
A;Residues: 1-448 <WOO>
A;Cross-references: EMBL:AL022117; PIDN:CAA17931.1; GSPDB:GN00067; SPDB:SPBC119.16c
A;Experimental source: strain 972h-; cosmid c119
                                                                                                                                                                                                                                                                                R;Wood, V.; Rajandream, M.A.; Barrell,
submitted to the EMBL Data Library, Ma:
A;Reference number: Z21843
                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SPBC119.16c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Molecule type: DNA
A;Residues: 1-357 <DOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AF083031; NID: g13794284; PIDN: AAK39661.1;
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                                                                                                                                                    Gene:
                                                       45.2%;
Local Similarity 47.4%;
nes 9; Conservation
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Pred. No.
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                                                                                  Score 47; DB Pred. No. 13;
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Pred. No.
 27
                                                                                                                                                                                                                                                                                                                                                                                      fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                     ll, B.G.; Skelton,
March 1998
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A;Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457 R;KOhsaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka, K.; Miyamoto, J. Clin. Invest. 85, 1566-1574, 1990 A;Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct au A;Reference number: I55553; MUID:90237237; PMID:1692037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 45-97,'LK' <CH3>
A;Cross-references: GB:J04205
A;Cross-references: GB:J04205
A;Note: this sequence has been revised in reference A31888
R;Nyman, U: Ringertz, N.R.; Pettersson, I.
Immunol. Lett. 22, 65-72, 1999
A;Title: Demonstration of an amino terminal La epitope recognized by human anti-La
A;Reference number: A61051; MUID:89379261; PMID:2476379
A;Accession: A61051
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A; Residues: 1-19, E', 21-47 < NYM>
A; Residues: 1-19, E', 21-47 < NYM>
R; Sturgess; A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, R.
J. Immunol. 140, 3212-3218, 1988
A; Title: Characteristics and epitope mapping of a cloned human autoantigen La.
A; Reference number: S11013; MUID:88199081; PMID:2452201
A; Accession: S11013
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDNA clones expressing
A;Reference number: A22956; MUID:85166283; PMID:3856888
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A; Introns: 22/3;
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A; Residues: 'E', 55-287, 'V', 289-408 <STU>
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A; Residues: 1-408 < CH2>
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A;Residues: 174-224 <RE2>
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A; Residues: 81-107 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Molecule type: mRNA;
;Residues: 279-342 <RE3>;Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497;Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497;Comment: This protein associates with a variety of small RNA molecules, most of which;Comment:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: ribonucleoprotein La; rik; Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Gene: GDB:SSB
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Best Local
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bonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                        Conservative
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RNA-binding RNP2 motif
RNA-binding RNP1 motif
                                                                                                                                                                                                                               85.1%;
94.7%;
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Pred. No. 3
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ribonucleoprotein La.A - African clawed frog
N;Alternate names: aucoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb_1994 #sequence_revision 26-May-1994 #text_change
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RESULT 3

22-Jun-1999

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RESULT 4
S33817
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A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection A;Reference number: JC1494; MUID:93246255; PMID:7916708
A;Accession: JC1494
                                                                                                                                                                                                                                                                             C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat C;Keywords: phosphoprotein; RNA binding F;111-177/Domain: ribonucleoprotein repeat homology <RRM> F;112-117/Region: RNA-binding RNP2 motif F;150-157/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: La proteins from Xenopus laevis. cDNA cloning and A;Reference number: S33817; MUID:93287095; PMID:8510143 A;Accession: S33817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonucleoprotein La B - African clawed frog
N,Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: S33817; S28544
R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: phosphoprotein; RNA binding
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A;Residues: 1-415 <SEM>
A;Cross-references: GB:X67859; NID:g55778; PIDN:CAA48043.1; PID:g55779
A;Experimental source: liver
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C;Species: Rattus norvegicus (Norway rat)
RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                   ay act as a transcription termination factor
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                                                                                                                3 LEAKICHQIEEYYFGD 18
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RNA-binding RNP2 motif
RNA-binding RNP1 motif
                                                                                                                                                                                                                                                          phosphorylated
                                                                                                                                                                                       57.2%;
75.0%;
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94.7%;
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Pred. No. 3.6e-06;
                                                                                                                                                                                       Score 59.5;
Pred. No. 0.
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                                                                                                                                                                                                                                                            predicted <PHY>
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                                                                                                                                                                                                             DB 1; Length 427;
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Run on: OM protein - protein search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Scoring table: Sequence: Title: Perfect score: Database : Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: Searched: PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* September 10, 2004, 17:33:11; Search time 14.8603 Seconds (without alignments)
122.988 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-836-073-16 104 283366 seqs, 96191526 residues 1 AALEAKICHQIEEYYFGDF 19 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 283366

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	σ	4	ω	N	ı	Result No.
42	42	42	43	43	43	43	44	44	45	4 5	45	45	45	45	45	45	46	46	47	47	47	47	55		59.5	•	88.5	88.5	Score
40.4	40.4	40.4	41.3	41.3	41.3	41.3	42.3		43.3			•		43.3		43.3		44.2	45.2		45.2		•	53.4	•		85.1	85.1	Query Match
428	421	386	609	510	427	88	564	552	1164	1164	1164	1164	1164	1156	620	409	456	352	482	448	357	187	135	428	427	415	408	404	Length
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hypothetical prote	æ	hypothetical prote	nodulation factor	glucose-1-phosphat	probable desA3 pro	conserved hypothet	carboxylesterase (carboxylesterase (A24R protein - var	A25R protein - var	RNA	RNA		RNA polymerase sub	acetylcholinestera	eukaryotic release	hypothetical prote	probable membrane					thioredoxin - Aqui	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	Description

ALIGNMENTS

RESULT 2 A31888 ribonucleoprotein La - human ribonucleoprotein SS-B; Sjogren syndrome antige. C;Species; Homo sapiens (man) C;Date: 21-May-1990 #sequence revision 26-May-1994 #text_change 22-Jun-1999 C;Date: 21-May-1990 #sequence revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: A31888; S03948; \(\overline{A22956}\); A61051; S11013; I55\(\overline{5}\)3; I70205; I70206; A31273 R;Chambers, J.C; Kenan, D.; Martin, B.J.; Keene, J.D. J. Biol. Chem. 263, 18043-18051, 1988 A;Title: Genomic structure and amino acid sequence domains of the human La autoantigen. A;Reference number: A31888; MUID:89053970; PMID:3192525 A;Accession: A31888 A;Molecule type: mRNA A;Residues: 1-408 < CHA> A;Cross-references: GB:J04205; NID:9178686; PIDN:AAA51885.1; PID:9178687 R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989 A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences	Query Match 85.1%; Score 88.5; DB 1; Length 404; Best Local Similarity 94.7%; Pred. No. 3.5e-06; Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1; Qy 1 AALEAKICHQIEEYYFGDF 19	A; Molecule type: mRNA A; Residues: 1-404 < CCHA- A; Residues: 1-404 < CCHA- A; Cross - references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A; Oross - references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A; Note: part of this sequence was confirmed by protein sequencing C; Comment: This protein associates with a variety of small RNA molecules, most of which C; Comment: This protein termination factor. C; Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C; Keywords: blocked amino end; phosphoprotein; RNA binding F; 112-178/Domain: ribonucleoprotein repeat homology < RRM> F; 113-118/Region: RNA-binding RNP2 motif F; 151-158/Region: RNA-binding RNP1 motif F; 228-404/Domain: phosphorylated #status predicted < PHY>	RESULT 1 \$03849 ribonucleoprotein La - bovine N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: \$03849 R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989 A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences A;Accession: \$03848; MUID:89202037; PMID:2468131 A;Accession: \$03849

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Search completed: September 10, 2004, 18:11:56 Job time : 41.424 secs

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GENERAL INFORMATION:

APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.

APPLICANT: Das, S.

APPLICANT: Das, S.

APPLICANT: Daidya, Narayan
ITITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
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US-09-836-073-11
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-9
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                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09836073
Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12
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                                                                                                                  APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
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Local Similarity 80.0%;
Les 12; Conservative
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Pred. No. 0.0015;
1; Mismatches
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Pred. No. 0.00075;
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US-09-836-073-16
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                                                     Query Match
Best Local Similarity
Matches 13; Conserv
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PRIOR ETLING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 19
TYPE: PRT
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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APPLICANT: Das, S.
APPLICANT: Bais, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
FURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                        APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054852
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
CURRENT FILING DATE: 2002-10-24
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75.0%;
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                                                            Score 65.5; DB 9
Pred. No. 0.0039;
1; Mismatches
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Pred. No. 0.0022;
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Pred. No. 0.0015;
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                                                                                          DB 9; Length 19;
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US-10-102-806-695
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US-10-102-806-695
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; ORGANISM: Homo sapiens
US-10-264-049-2643
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Best Local Similarity
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2643
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2643, Application US/10264049 Publication No. US20040005579A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 695
LENGTH: 460
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                                                                  Query Match
Best Local Similarity
Matches 13; Conserv
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                               APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: ECT/US01/18569
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
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                                                                                                                                                                                              LENGTH: 460
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                           LDTKICEQIEYYFGDF 18
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LEAKICHQIEYYFGDF 80
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                                                                    Conservative
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81.2%;
                                                                                      76.0%; Score 76; DB 15; Length 460; 81.2%; Pred. No. 0.0026;
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Pred. No. 0.0026;
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RESULT 9
US-09-836-073-2
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-2
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                                                                                                                                  RESULT 11
US-09-836-073-9
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US-09-836-073-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL RE:
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
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APPLICANT: Dasgupta, Asim
                                                                       Sequence 9, Application US/09836073 Patent No. US20020173475A1 GENTRAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
LENCTH: 18
TYPE: PRT
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Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                           Local
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l Similarity 80.0%;
12; Conservative
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Similarity 75.0%;
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   TO INHIBIT VIRAL REPLICATION
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Pred. No. 0.00018
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Pred. No. 0.00037;
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; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Das S.
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
                                                           Sequence 14, Application US/09836073

Patent No. US20020173475A1

GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Dasidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION UNMEER: US/09/836,073
CURRENT APPLICATION NUMBER: US/09/836,073
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PLING DATE: 199-05-21
PRIOR FILING DATE: 199-05-21
PRIOR FILING DATE: 199-05-21
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 18
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Matches
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Best Local Similarity 81.2%;
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13; Conserv
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81.2%; Pred. No. 9.16
tive 1; Mismatches
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Pred. No. 8.
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; TYPE: PRT
; ORGANISM: Bovine
US-09-836-073-14
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; ORGANISM: Homo Sapiens
US-10-170-385-477
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                     NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Sequence 695, Application US/09925298
Publication No. US20020039764A1
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Best Local Similarity
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Matches 13; Conserv
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APPLICANT: Mundy, Christopher
APPLICANT: Kan, On
APPLICANT: Harris, Robert Ale
APPLICANT: White, Jonathan
                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                     APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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ORGANISM: Homo sapiens
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                                    ENGTH:
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Rayner, William Nigel
Naylor, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsman, Susan Mary
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81.2%;
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81.2%;
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Pred. No. 9.1e-05;
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Pred. No. 0.0023;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

15: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

17: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

18: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

19: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*
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143.151 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-836-073-15
100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDLDTKICEQIEYYFGDF 18
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

15	14	13	12	11	10	ø	œ	7	თ	U	4	ω	N	1	No.
65.5	67	89	68	70	72	74	76	76	76	76	76	76	76	100	Score
65.5	67.0	68.0	68.0	70.0	72.0	74.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	100.0	Match
19	18	18	18	18	18	18	460	460	460	408	18	18	17	18	Match Length DB
9	9	9	9	9	9	9	15	14	12	12	9	ø	9	9	<u> </u>
US-09-836-073-16	US-09-836-073-10	US-09-836-073-12	US-09-836-073-11	US-09-836-073-9	US-09-836-073-4	US-09-836-073-2	US-10-264-049-2643	US-10-102-806-695	US-09-925-298-695	US-10-170-385-477	US-09-836-073-14	US-09-836-073-1	US-09-836-073-13	US-09-836-073-15	ID
Sequence 16, App1	Sequence 10, Appl	Sequence 12, Appl	Sequence 11, Appl	Sequence 9, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2643, Ap	Sequence 695, App	Sequence 695, App	Sequence 477, App	Sequence 14, Appl	Sequence 1, Appli	Sequence 13, Appl	Sequence 15, Appl	Description

ALIGNMENTS

```
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 18
                                      RESULT 2
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Xenopus US-09-836-073-15
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US-09-836-073-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/09836073 Patent No. US20020173475A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 100; DB 9
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches
APPLICANT: Dasgupta, Asim APPLICANT: Das, S.
                                                                                                                                                                                                                        1 LDLDTKICEQIEYYFGDF 18
                                                                                                                                                                                               1 LDLDTKICEQIEYYFGDF 18
                                                                                                                                                                                                                                                                                                                                  DB 9;
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                                                                                                                                                                                                                                                                                                                                  Length 18;
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PRIOR APPLICATION DATA:

-----N NIMBER: US 08/844,419

FILING DATE:

18-APR-1997

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RESULT 15
US-09-430-323-24
; Sequence 24, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relev
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-854-050-24
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION NUMBER: US/09/430,323
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/861,843
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ICHQ-EYYFGDF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICEQIEYYFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, 8th Floor
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                           Best Local Similarity 83.3%; Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                  7 ICEQIEYYFGDF 18
ICHQ-EYYFGDF 11
                                                                                                                                                                                                                                      LENGTH: 37 amino acids
TYPE: amino acid
                                                                         0; Mismatches
                                                                                        Score 50.5; DB 4;
Pred. No. 0.21;
                                                                         1;
                                                                                                         Length 37;
                                                                         Indels
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Search completed: September 10, 2004, 18:05:10 Job time : 16.8883 secs

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LING DATE:

08/851,843

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS:
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                           TITLE OF
                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                     COUNTRY:
                                             APPLICATION NUMBER: US/0
            CLASSIFICATION:
IOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
SEQUENCE DESCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                       T: Andrews, William H.
INVENTION: No. 609380
F SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICHOXEYYFGDF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997 APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08851843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICATION NUMBER: US 08/912,951
TLING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LING DATE:
                                                                                                                                                                                                                                                                                                                                                         Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                        Lingner, Joachim
Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                          Chapman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                             Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.0%;
                                                                                                                                                                                                                                                                                                                                                                                              Karen B.
                                                               US/08/851,843A
US 08/846,017
                                                                                                                                                                                                                                                                                                                           6093809el Telomerase
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Pred. No. 0.0063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                    Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214:
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US-08-854-050-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
TENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, App. --- No. 6261836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                    PRIOR APPLICATION NUMBER: US 08/851,...
PILING DATE: 06-WAX-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                   AFFILICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                    APPLICATION NUMBER: 1
FILING DATE: 09-MAY-
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
APPLICATION NUMBER: FILING DATE: 25-APPLICATION: 53
                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                       9411:
                                                                                                                                                                                                                                                                                                                                      San Francisco
: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08854050
                                                                                                                                                                                                                                                                                                                                                                         E: Townsend and Townsend and Crew Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                    United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lingner, Joachim
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                                                                                                                                                           09-MAY-1997
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                  25-APR-1997
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83.3%;
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
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; MOLECULE TYPE: peptide US-08-974-549A-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 214, Application US/09402181B Patent No. 6610839 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: F1DPDY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Vers

SOFTWARE: PATENTIN Release #1.0, Vers

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                         APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
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Harley, Calvin B.
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14-AUG-1997
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Pred. No.
US 08/854,050
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0.0063;
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US-09-721-456-214
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Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-No. 6617110-2000

CIACGERICATION. "IN-COMPATION OF THE PATENT APPLICATION OF THE PATENT 
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                      PRIOR
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TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                   CLASSIFICATION: <Unknown>
R APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-MOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
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                            APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
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83.3%;
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   US 08/846,017
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Pred. No. 0.0063;
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US-09-721-456-215
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Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                        APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997
                                                                                                                                                APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/974,549AFILING DATE: 19-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                        APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/911,312 PILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                      ILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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Chapman, Karen B.
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US-08-974-549A-214
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Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                     CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APPL-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
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                                   FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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 APPLICATION NUMBER: FILING DATE: 14-AU
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
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    T: Harley, Calvin B.
    T: Andrews, William H.
    INVENTION: Human Telomerase Catalytic Subunit

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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Chapman, Karen B.
Morin, Gregg B.
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UMBER: US 08/912,951
14-AUG-1997
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                                                      14-AUG-1997
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                                                                         US 08/911,312
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Pred. No.
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. 0.0014;
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RESULT 7
US-09-430-323-25
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Best Local Similarity
Warrches 11; Conserva
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                                                                           TELEFAX: (415) 576-0: INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No.
                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/430,323 FILING DATE: 29-Oct-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
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                                       TYPE: amino acid
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                                                         LENGTH: 38 amino acids
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Harley, Calvin
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not relevant
relevant
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0.0014;
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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25
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GENERAL INFORMATION:
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Best Local Similarity
                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                    REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                     SEQUENCE CHARACTERISTICS:
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                                                                                 TELEPHONE:
                                                                                                                                                                    NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: US 08/911,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/724,643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDRESSEE: Townsend and Townsend and Crew LLF
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Chapman, Karen B.
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38 amino acids
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                                                                                 (415) 576-0200
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Matches

11;

Conservative

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Mismatches

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7 ICEQIEYYFGD 17

Query Match Best Local Similarity

64.0%; Score 64; DB 3; 100.0%; Pred. No. 0.0014;

Length 38; ; ; ; Indels

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                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                            APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA:
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                                                                                                   PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two .... CITY: San Francisco
                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 14-AUG
                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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LICATION NUMBER: US 08/851,843
JING DATE: 06-MAY-1997
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Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                  UMBER: US 08/915,503
14-AUG-1997
                                                                                                                                                                                                                                                                                                                             UMBER: US 08/854,050
09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US 08/844,419
18-APR-1997
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                            Randolph
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14-AUG-1997
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NUMBER: 015389-002610US
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Iwo CITY: San Francisco
STATE: California
****ired State
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                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 18-APR-
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
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                                               ATTORNEY/AGENT INFORMATION: NAME: Apple, Randolph T
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NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE DOCKET NUMBER: 015389-002930US

REFERENCE DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palan-
                                                                                                                                                                                                           FILING DATE: 25 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997
                                                                              FILING DATE: 01
CLASSIFICATION:
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Harley, Calvin
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Chapman, Karen B.
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100.0%; Pred. No. 0.0
tive 0; Mismatches
                                                                                                               US 08/724,643
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1997-10-06

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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-10
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-05
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Harley
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                                                                  TELEFAX: (404)-873-87
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS; single
                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: January
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                      NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08 FILING DATE: June 7, 1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: GA
                                                                                                    TELEPHONE:
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ຕິດ 664181
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                                                                  : (404)-0;
(404)-873-8795
TD NO: 20:
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                                                                                                                                                                                                                                                         January 31, 1991
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81.2%;
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                                                                                                                                                   31,284
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Pred. No. 7.4e-06;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
TOPOLOGY: n
                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
                                                                                                                                                  NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 01-OC CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLE OF INVENTION:
                           STRANDEDNESS:
                                           TYPE: amino acid
                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                          FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
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Andrews, Willi
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Chapman, Karen B.
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               not relevant
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8..15
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                                                                                    5) 576-0300
576-0300
25:
                              not relevant
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91.7%;
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No. 6093809el Telomerase
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Pred. No. 0.00051;
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Result
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Perfect score:
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                50.5
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Gapop 10.0 ,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
  Copyright
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            sw model
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58.488 Million cell updates/sec
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Compugen Ltd
Sequence 3, Appli
Sequence 4, Appli
Sequence 20, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 215, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 276, Appl
Sequence 3800, Appli
Sequence 4, Appli
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40 40.0 775 3 US-09-281-259-4 40 40.0 1956 3 US-08-843-417-2 40 40.0 1956 3 US-08-843-417-10 40 40.0 1956 4 US-09-527-013-2 40 40.0 1956 4 US-09-527-013-2 40 40.0 1956 4 US-09-527-013-10 40 40.0 1956 4 US-09-527-013-10 40 40.0 1956 4 US-09-527-013-2 40 40.0 1956 4 US-09-527-013-2 40 40.0 1956 4 US-09-527-013-2 40 40.0 1956 4 US-09-721-456-191 40 39 39.0 83 3 US-08-851-843A-191 41 39 39.0 85 3 US-08-851-843A-11 42 39 39.0 85 3 US-08-851-843A-11 43 39 39.0 85 3 US-08-851-843A-11 43 39 39.0 85 3 US-08-854-050-11 45 39 39.0 85 3 US-08-854-050-11 46 40.0 1956 3 US-09-423-11 47 39 39.0 85 4 US-09-430-233-11 48 39 39.0 85 4 US-09-421-818-193 48 39 39.0 85 4 US-09-721-456-193	45	44	43	42	41	40	39	38	37	36	35	ω 4	33	32	31	30	29
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US-09-281-259-4 US-08-843-417-2 US-08-843-417-10 US-09-527-013-2 US-09-527-013-10 US-08-851-843A-9 US-08-854-050-9 US-09-402-181B-191 US-08-851-843A-11 US-09-721-456-191 US-08-854-050-11 US-08-854-050-11 US-09-402-181B-193 US-08-854-050-11 US-09-402-181B-193 US-08-854-050-11 US-09-402-181B-193 US-08-854-050-11 US-09-430-323-11 US-09-430-323-11	4	4	Α,	w	w	ω	4	4	4	w	w	w	4	4.	ω	ω	ω
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RESULT 1

ALIGNMENTS

US-09-316-630-3 멼 S US-09-316-630-3 SOFTWARE: PA SEQ ID NO 3 LENGTH: 18 TYPE: PRT GENERAL INFORMATION: APPLICANT: Das, Sa APPLICANT: Dasgupt sequence 3, Application US/09316630 Patent No. 6291637 Query Match Best Local (Matches APPLICANT: DASGUPTA, ASIM TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS FILE REFERENCE: 22000-20548.21 CURRENT APPLICATION NUMBER: US/09/316,630 CURRENT FILING DATE: 1999-05-21 PRIOR APPLICATION NUMBER: 08/817,953 PRIOR APPLICATION NUMBER: 08/321,427 PRIOR FILING DATE: 1997-10-06 PRIOR APPLICATION NUMBER: 08/321,427 PRIOR APPLICATION NUMBER: 08/321,427 PRIOR APPLICATION NUMBER: 08/321,427 PRIOR APPLICATION NUMBER: 09/086,527 PRIOR FILING DATE: 1998-NUMBER OF SEQ ID NOS: 4 ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: 13; 3 LDTKICEQIEYYFGDF 18 |: ||| ||||||| w Similarity PatentIn Ver. LEAKICHQIEYYFGDF Das, Saumitra Conservative 1998-05-22 76.0%; Score 76; 81.2%; Pred. No. Mismatches 7.4e-06; DB 3; Length 18; Indels 0 Gaps 0

US-09-316-630-4

Sequence 4, Application US/09316630 Patent No. 6291637

GENERAL INFORMATION:
APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERPERENCE WITH VIRAL
TITLE OF INVENTION: SMALL YEAST RNA REVEALS
FILE REFERENCE: 22000-20548.21

IRES-MEDIATED TRANSLATION BY A CRITICAL RNA-PROTEIN INTERACTIONS

CURRENT APPLICATION NUMBER: US/09/316,630 CURRENT FILING DATE: 1999-05-21 PRIOR APPLICATION NUMBER: 08/817,953

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Best Local
PIR; Ts/411; 13/41.

GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003679; F:DNA-directed RNA polymerase act
GO; GO:0003900; F:DNA-directed RNA polymerase II a
GO; GO:0003901; F:DNA-directed RNA polymerase II:
GO; GO:0003901; F:DNA-directed RNA polymerase II:
GO; GO:0003902; F:DNA-directed RNA polymerase II:
GO; GO:0003902; F:DNA-directed RNA polymerase II:
GO; GO:00036740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR007645; RNA_pol Rpb2 3.
InterPro; IPR007646; RNA_pol Rpb2 4.
InterPro; IPR007646; RNA_pol Rpb2 5.
InterPro; IPR007647; RNA_pol Rpb2 5.
InterPro; IPR007647; RNA_pol Rpb2 6.
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EMBL; AY050403; AAK91419.1; -
EMBL; BT000588; AAN18157.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; C:nucleus_IEA.
InterPro; IPR006304; Lupus_La.
InterPro; IPR006304; Lupus_La.
InterPro; IPR006630; Lupus_La.
InterPro; IPR006630; Lupus_La.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR006504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF05383; La; 1.
PRINTS; PR00376; xrm; 1.
SMART; SM00370; RNM; 1.
SMART; SM00370; RNM; 1.
PROSITE; PS50102; RRM; 1.
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SEQUENCE FROM N.A.
Cheuk R., Chen H.,
Chan M.M., Chang
                                                                                              EMBL; U94848;
PIR; T37411;
GO; GO:000367
GO; GO:000389
GO; GO:000390
GO; GO:000390
GO; GO:000390
GO; GO:000590
GO; GO:000590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O57230 PRELIMINARY; PRT; 1156 AA.
O57230;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA polymerase subunit rpo132 (EC 2.7.7.6) (DNA-directed polymerase beta chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chen K., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
Southwick A., Tang C.C., Toriumi M., Wallender B.K., Wong C., Wu H.C.,
Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                  Submitted (MAR-1997) to -1- CATALYTIC ACTIVITY: {RNA}(N)
                                                                                                                                                                                                                                                                                                       strain."
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Ankara;
Antoine G., Scheiflinger F.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinia virus (strain Ankara)
Viruses; dsDNA viruses, no RNA
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                                                                                                                                                                                                                                                                                                                      "The complete genomic
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                                                                                                                                                                                                                    U94848; AAB96526.1;
T37411; T37411.
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N NUCLEOSIDE TRIPHOSPHATE = N DI
                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA stage;
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Pred. No.
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ce of the Modified Vaccinia Ankara
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e I activity; IEA.
e II activity; IEA.
e III activity; IEA.
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Fizaki Y.,
Finn G.,
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RESULT 15
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                                                                   PIR; T2556; T28566.

GO; GO:0003677; F:DNA-directed RNA polymerase act GO; GO:0003899; F:DNA-directed RNA polymerase I a GO; GO:0003901; F:DNA-directed RNA polymerase II a GO; GO:0003901; F:DNA-directed RNA polymerase II GO; GO:0003902; F:DNA-directed RNA polymerase III GO; GO:0003902; F:DNA-directed RNA polymerase III GO; GO:0006350; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0006350; P:transcription; IEA.

InterPro; IPR007645; RNA pol Rpb2 3.

InterPro; IPR007647; RNA pol Rpb2 5.

InterPro; IPR007647; RNA pol Rpb2 7.

R Ffam; PF04566; RNA pol Rpb2 3; 1.

Pfam; PF04566; RNA pol Rpb2 3; 1.

Pfam; PF04566; RNA pol Rpb2 5; 1.

Pfam; PF04560; RNA pol Rpb2 7; 1.

R PROSITE; PS01166; RNA pol Rpb2 7; 1.
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Best Local Similarity
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Best Local (
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Pfam; pF04565; RNA_pol_Rpb2_4; 1.
Pfam; pF04565; RNA_pol_Rpb2_4; 1.
Pfam; pF04567; RNA_pol_Rpb2_5; 1.
Pfam; pF04567; RNA_pol_Rpb2_6; 1.
Pfam; pF04560; RNA_pol_Rpb2_7; 1.
Pfam; pF04560; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_pol_Rpb2_7; 1.
PNOSITE; PS01166; RNA_pol_Rpb2_7; 1.
DNA-directed RNA_pol_WETA; 1.
DNA-directed RNA_pol_WETA; 1.
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Q90027;
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MEDLINE=94088747; PubMed=8264798;
Massung R.F., Esposito J.J., Liu L., Qi J.,
Knight J.C., Aubin L., Yuran T.E., Parsons
Selivanov N.A., Cavallaro K.F., Kerlavage J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, 25R (EC 2.7.7.6) (DNA-direc
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            smallpox virus genome.";
Nature 366:748-751(1993)
-!- CATALYTIC ACTIVITY:
{RNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=12870;
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Viruses, dsDNA viruses,
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"Potential virulence determinants
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Last annotation update)
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Score 53; DB
Pred. No. 11;
2; Mismatches
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Pred. No. 11;
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polymerase I activity; IEA.
polymerase II activity; IEA.
polymerase III activity; IEA
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B8101B CRC64;
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RESULT
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Best Local Similarity
Matches 9; Conserv
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STRAIN=Reynolds and Newman;

STRAIN=Reynolds and Newman;

Bagga N., Wann E.R., Foster T.J., Lee J.C.;

Bagga N., Wann E.R., Foster T.J., Lee J.C.;

Bagga N., Wann E.R., Foster T.J., Lee J.C.;

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U81973; AAC46099.1; -.

HSSP: P27828; 1F6D.

GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;

GO; GO:0008761; P:UDP-N-acetylglucosamine metabolism; IEA.

GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.

InterPro; IPR00333; Epimerase_2; 1.

Pfam; PF03250; Epimerase_2; 1.

TIGRFAMs; TIGR00236; WecB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O99X57; PRELIMINARY; PRT; 391 AA.
099X57; O1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Capsular polysaccharide synthesis enzyme Cap5P.
CAPP OR SAV0164 OR SA0159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus type 5 capsular polysaccharide."; Mol. Microbiol. 27:9-21(1998).
                                                                                                                                                                                                                                                                                                                 InterPro; IPR003331; Epimerase 2.

Pfam; PR02550; Epimerase 2; 1.

TIGRFAMs; TIGR00236; wecB; 1.

Complete proteome.

SEQUENCE 391 AA; 44372 MW; DOI
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HSSP, P27828; 1F6D.

GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;

GO; GO:0009103; P:Ulpopolysaccharide biosynthesis; IEA.

GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP003358; BAB56326.1; -. EMBL; AP003129; BAB41379.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jancet 357:1225-1240(2001).
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366
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RICEALEYYFG
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Pred. No. 2.8;
1; Mismatches
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Pred. No. 2.8;
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Q9FL36;
01-MAR-2001
01-MAR-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q94A38;
Q94A38;
01-DEC-2001
Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Mey Shinn P., Chen H., Carninci P., Dale J.M., Goldsmith Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiy Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Arabidopsis cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. features of the regions of 1,381,565 bp covered by twenty c physically assigned P1 and TAC clones.";
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel. 16, Last as
01-CCT-2003 (TrEMBLrel. 25, Last as
Similarity to RNA-binding protein.
                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
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InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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56.2%;
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Last sequence update)
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dons; core eudicots; rosid
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            databases.
                                                                                                                            Lin J., Liu S.X.,
S., Palm C.J.,
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                                                                                                           Southwick A.,
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Best Local
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GO; GO:0000761; F:UDP-N-acetylglucosamine 2-epimerase activity; GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.

GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.

InterPro; IPR003331; Epimerase_2.

Pfam; PF02350; Epimerase_2; 1.

TIGREAMS; TIGR0236; wecB; 1.

Complete proteome.

SEQUENCE 381 AA; 43106 MW; 125E4D5D19047707
                                                                                        P72382;
P72382;
01-FEB-1997
01-FEB-1997
01-JUN-2003
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Pfam; PP05383; La; 1.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS01118; SUI1 1; 1.
SEQUENCE 826 AA; 91377 MW;
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EMBL; AY139801; AAM98107.1; --
EMBL; AC14997; AAO73903.1; --
GO; GO:0003743; F:translation initiation fac
GO; GO:0006413; P:translational initiation;
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR001950; TIF_SUII.
                   Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants
acquired MRSA,",
Lancet 359:1819-1827(2002).
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MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa
Nagai Y., Iwama N., Asano K., Naimi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus Bacteria; Firmicutes;
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01-JUN-2003 (TrEMBLrel.
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01-OCT-2002
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    Firmicutes;
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Bacillales; (
  Bacillales;
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Pred. No.
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    Staphylococcus
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Kuroda H., Cui L
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2.7;
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on; IEA.
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AC P95709
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Matches
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P95709;
01-MAY-1997
01-MAY-1997
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                                                                                                                                            J. Bacteriol.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                Microbiology 143:0-0(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97197525;
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9; Conservative
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"Molecular characterization and transcriptional analysis capsule genes in Staphylococcus aureus.";
J. Bacteriol. 179:1614-1621(1997).

EMBL; U73374; AAB49445.1; -.

HSSP; P27828; 1F6D.

HSSP; P27828; F:UDP-N-acetylglucosamine 2-epimerase act GO; GO:0009103; F:lipopolysaccharide biosynthesis; IEA.

GO; GO:000647; P:UDP-N-acetylglucosamine metabolism; IEA.

InterPro; IPR003331; Epimerase 2.

Pfam; PF02350; Epimerase 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96178981; PubMed=8606192;
Sau S., Lee C.Y.;
"Cloning of type 8 capsule genes and analysis of
production of different capsular polysaccharides
                                                                                                                                                                                                                                                                                                                                                                                                              178:2118-2126(1996).
                                                                           44247 MW;
                  54.0%;
81.8%;
                  Score 54;
Pred. No.
                                                                           1E8D9FAA9BC76F0D
Mismatches
                  DB:
                                    2;
                                    Length 391;
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(TrEMBLrel. 03, (TrEMBLrel. 03, (TrEMBLrel. 24, Bacillales; Staphylococcus Last sequence update)
Last annotation update) Created) sequence update) 391 Å

SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Reynolds and Newman;
STRAIN=Reynolds and Newman;
STRAIN=897388587; PubMed=9245821;
MEDLINE=97388587; PubMed=9245821;
Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.;
Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.;
The Staphylococcus aureus allelic genetic loci for serotype 5
"The Staphylococcus aureus allelic genetic loci for serotype 5 5 and 8 common

STRAIN=Reynolds and Newman;
MEDLINE=98101481; PubMed=9440531;
Kiser K.B., Lee J.C.;

[3]
SEQUENCE FROM N.A.
STRAIN=Reynolds and Newman;
STRAIN=898125727; PubMed=9466251;
MEDLINE=98125727; PubMed=9466251;
Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee
Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee "Staphylococcus aureus cap50 and cap5P genes functionally complement mutations affecting enterobacterial common-antigen biosynthesis in Escherichia coli."; 180:403-406(1998) Lee Ċ

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09:36:13

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Sammons L.,
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RESULT 6
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Matches 11
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EMBL; BC045392; AAH45392.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La.
InterPro; IPR00564; RNA_rec_mot.
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01-JUL-1997
01-OCT-2003
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to sjogren syndrome antigen B (Autoantigen La).
Brachydanio rerio (Zebrafish) (Danio rerio)
Eukaryota: Metazo
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                           "Genome sequence of the new investigating biology. The Science 282:2012-2018(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7ZTI0
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                   "The sequence of C. Submitted (MAY-1997)
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Pred. No.
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Q940X9;
Q1940X9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OEC-2003 (TrEMBLrel. 25, Last annotation update)
AT592T160/T10F18_190 (Proline-rich protein family).
                                                                                                                                                                                                                                                                                                                                                            Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick Jrang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Bavis R.W., Theologis A., Ecker J.R.; "Arabidopsis CDNA clones.";
SEQUENCE FROM N.A.

STRAIN-cv. Columbia;

Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Ronning Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., VanAken Feldblyum T.V., Yu C., Wortman J.R., White O., Fraser C.M.;

"Arabidopsis thaliana chromosome 5 BAC F13M11 genomic sequence.";

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                               Nguye...
Southwick A., ran-
                                                                                                                                                                                    Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Chan V.W., Ishida J., Jones T., Kamiya A., Kariin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H. Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosiceurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS00030; RRM_RNP_1; I
SEQUENCE 396 AA; 43631 MW;
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WormPep; C44E4.4; CE08718.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Shinn P., Chen H.,
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                        "Arabidopsis ORF clones.";
Submitted (AUG-2002) to the
                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
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                                                                                                                                         EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FALSE NEG
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                                                                                                                                         databases
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 13
                                                                                                                                                                                        Q8BTU4;
01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Sjogren syndrome antigen B.
                 Bukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SEQUENCE 381 AA; 43891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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01-JUN-2001
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                                                                                                                                                            Sjogren syndrome
                                                                                                                                                                                                                                                                                                    Q8BTU4
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MGD; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus; IDA.
INterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
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                                                                                                                                                                                     (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                              antigen
                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.
43891 MW;
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81.2%;
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25,
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Last annotation update)
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                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                  Last sequence update)
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Pred. No.
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                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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RESULT 4
Q8QHI5
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Best Local S
Matches 11
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                           L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMBL/GenB
EMBL; AR467897; AAL76269 1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La.
Cheen. EDGC502.11.1.
                                                                                                                                                                                            PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8QHI5 PRELIMINARY; PRT; 206 AA.
Q8QHI5;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Untranslated region binding-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; PROSOLO; REM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1
PROSITE; PS00030; RRM RNP_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus;
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PS00030; RRM RNP_1; 1.
206 AA; 23992 MW;
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                          LDTKICEQIEYYFGD 17
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LESKICQQIEYYFGN
                                                                                                   Conservative
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81.2%;
                                                                                                                        68.0%;
73.3%;
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27
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                                                                                                   4
                                                                                                Score 68; DB
Pred. No. 0.00
4; Mismatches
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Pred. No. 0.001;
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                                                                                                                                                                                                    965B62F7DFFB90E9 CRC64;
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                                                                                                                        DB 13;
0.0092;
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                                                                                                   <u>,</u>
                                                                                                                                               Length 206;
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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and
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                                                                                                                                                              Score
                                                                                                                                                                                                        d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: sp_bacteria
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Q8BTU4
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Q8btu4 mus musculu
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Q8qhi5 gallus gall
Q7ztl0 brachydanio
O01806 caenorhabdi
         P72382 staphylococ
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O99X57 staphylococ
Q9f136 arabidopsis
Q9f138 arabidopsis
O57230 vaccinia vi
Q90027 variola maj
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Q8nyn8 staphylococ
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Q8AW24	Q7ZZ77	Q7ZZ53	Q8N3N2	Q8BN59	Q8C9A3	Q8CA51	Q9D3J0	Q9BRS8	Q9CTN3	Q8AW27	Q86R84	080567	Q8S0T8	044678	092455	P90691	Q7Z1R8	Q8T8V5	Q8RK98	Q90149	Q8GDD9	Q8B9G3	Q7VLE1	Q80DV1	Q8V2N1	Q8V4V3	Q8JL90	090031
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ALIGNMENTS

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RESULT 1
Q7ZTK2
ID Q7ZTK2
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AC Q7ZTK2;
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                                                                                                                       Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                   RIESUE=Embryo;

Klein S., Strausberg R.;

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC046654; AAH46654.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0003723; F:RNA binding; IEA.

InterPro; IPR002344; Lupus La.

InterPro; IPR006630; Lupus La.

InterPro; IPR006630; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                         Similar to lupus LA protein homolog B. Xenopus laevis (African clawed frog). Xenopus laevis (African clawed frog). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                             SEQUENCE
10 LDLDTKICEQIEYYFGD 26
               1 LDLDTKICEQIEYYFGD 17
                                                      l Similarity
17; Conserv
                                                                                                             427 AA; 48996 MW;
                                                      Conservative
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                                                                                  94.0%;
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                                                                     Score 94; DB 13; 
; Pred. No. 1.5e-06
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                                                                                                             1E7CD82D8AB9C69A CRC64;
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                                                                       1.5e-06;
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vaccinia

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THIC OR LA0980.

10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Thiamine biosynthesis protein thiC.

Q8F7G5; 10-OCT-2003

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STRAIN-56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

MEDLINE-22598143; PubMed-12712204;

MEDLINE-22598143; PubMed-12712204;

Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Zhang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-F., Wann M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                   Petroselinum crispum (Parsley) (Petroselinum hortense).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster:
campanulids; Apiales; Apiaceae; Apioideae; apioid superclade;
Apium clade; Petroselinum.
                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB011282; AAN48179.1; -. HAMAP; MF_00089; -; 1. InterPro; IPR002817; Thic. Pfam; PF01964; Thic; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 422:888-893(2003).
-!- FUNCTION: Required for th (HMP) moiety of thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leptospira interrogans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydroxymethylpyrimidine) (By similarity).-!- PATHWAY: Thiamine biosynthesis.-!- SIMILARITY: Belongs to the thiC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu J.-G., Zhao G.-P.;
"Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
                                                                                                                                                 4-hydroxylase) (CA4H) (C4H) CYP73A10 OR CYP73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01964; ThiC; 1.
ProDom; PD007048; ThiC; 1.
PIGRFAMS; TIGR00190; thiC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A.
                                 NCBI_TaxID=4043;
                                                                                                                                                                                                                                                                                        TOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thiamine biosynthesis; Complete proteome.
SEQUENCE 495 AA; 55989 MW; 1EB65456C99AA8A7 CRC64;
                                                                                                                                                                                                                                                                                     PETCR
                                                                                                                                                                                                                                                                                                                                                                                   333 VDLQTKICQEAPFY 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ! Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 1; Length 495; Pred. No. 6.2; indels 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                        PRT;
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Search completed: September 10, 2004, 17:53:07 Job time: 8.24022 secs

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"Modes of expression and common structural features of the complete phenylalanine ammonia-lyase gene family in parsley.";

Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995).

-!- FUNCTION: Controls carbon flux to pigments essential for pollination or UV protection, to numerous pytoalexins synthesized by plants when challenged by pathogens, and to lignins.

-!- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO01128; Cytochrome P450. Pfam; PF00067; P450; 1. PRING: PASO:
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Lignin biosynthesis.
-!- PATHWAY: Phenylpropanoid metabolism; second step.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Monooxygenase; Heme; NADP.
METAL 448 448 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SEQUENCE 506 AA; 58047 MW; 32F00EE959D69CCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L38898; AAC41660.1; -. PIR; T14907; T14907.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxycinnamate + NADP(+) + H(2)O.
215 SRLAQSFEYHFGDF 228
                                                                           5 TKICEQIEYYFGDF 18
                                                                                                                                                                                                         Similarity
                                                                                                                                                               6
                                                                                                                                                                    Conservative
                                                                                                                                                                                                         45.0%;
42.9%;
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                                                                                                                                                                                                         Score 45; DB 1; Pred. No. 9.3;
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RESULT 13
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ID LA DROME
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GN LA ORN
GN LA ORN
GN LA ORN
CO ENKAR
OC Neoppt
OC Neoppt
OC STRAI
RX MEDLI
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RX MEDLI
RX LA/SS
RI LA/SS
RI LA/SS
RI MO1.
RN [2]
RP SEQUE
RT homol
RT LA/SS
RI MO1.
RN [2]
RP SEQUE
RT HOMOL
RN [2]
RP SEQUE
RT GON
RT GION
RN [3]
RP SEQUE
RT GRON
RN [3]
RP SEQUE
RX MEDLI
RA MADII
RA MADII
RA Adam
RA MADII
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RA Adam
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RA Adam
RA ADOG
RA BOCK
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                 RX MEDLINE=20196006; PubMed=10731132;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Ghery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraza C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Merkhlov G.. Milshina N.V. Mobarry C.. Morris J. Moshrefi A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bai C., Li Z., Tolias P.P.;
"Developmental characterization of a Drosophila RNA-binding protein homologous to the human systemic lupus erythematosus-associated La/SS-B autoantigen.";
Mol. Cell. Biol. 14:5123-5129(1994)
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RNA-binding; Nuclear protein; DNA-binding.
DOMAIN 141 228 RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoo C.J., Wolin S.L.;
"La proteins from Drosophila melanogaster and Saccharomyces
cerevisiae: a yeast homolog of the La autoantigen is dispensable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Canton-S; TISSUE=Ovary; MEDLINE=94309632; PubMed=8035794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14:5412-5424(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8035818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44430 MW;
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   N.V., Mobarry C.,
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2.2;
   Morris J., Moshrefi
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A Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu X., Smith H.O.,
A Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                                                                                                                      CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0011638; La.
GO; GO:0008098; F:5S rRNA primary transcript binding;
GO; GO:0003723; F:RNA binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                            PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1;
RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                     PRINTS; PR00302; LUPUS SMART; SM00715; LA; 1.
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR009504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003666; AAF53885.1; -. PIR; A53773; A53773. PIR; A53781; A53781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U07652; AAA20518.1; -. EMBL; L32988; AAA21776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glands.
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
-!- SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: May be involved in transcription termination k polymerase III. Binds RNA and DNA. Binds to precursors c polymerase III transcripts. May play a specialized role development. SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo followed by a restricted pattern of mesodermal expression that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              later confined to the visceral mesoderm, gonads, gut, and
54
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                                                                   Similarity
8; Conser
                           ICEQIEYYFGD 17
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329
390
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182
                                                                    Conservative
                                                                                                                                         AA;
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169
183
283
329
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                                                                                 48.0%;
72.7%;
 64
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                                                                 Score 48; DB 1;
Pred. No. 2.2;
1; Mismatches
                                                                                                                                                        A -> R (IN REF. 1).
K -> N (IN REF. 1).
                                                                                                                                                                                            A -> T (IN REF. 1).
KH -> NS (IN REF. 1).
                                                                                                                                                                                                                               RNA-BINDING
                                                                                                                                                                                                                                                DNA-binding
                                                                                                                                         A8099288B90446A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hy L., Muzny D.M., Nelson D.L.,
Nusskern D.R., Pacleb J.M.,
                                                                                                                                                                                                                                 (RRM)
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••
                                                                                                      Length 390;
                                                                        Indels
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RESULT 14
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IPYR_MYCPU
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28-FEB-2003 (
28-FEB-2003 (
10-OCT-2003
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CONFLICT
SEQUENCE
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EMBL; L22858; AAA667;
PIR; A38499; HJNVAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      NP_BIND
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Helicase; DNA replication; ATP-binding; DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                    Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.; "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inorganic pyrophosphatase hydrolase) (PPase). PPA OR MYPU_4700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicase; DNA
Early protein
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21267165; PubMed=11353084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=UAB CTIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
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                                                                 This SWISS-PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR006824; Baculo_helicase.
European
by non-
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917
967
934
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(Rel. 41, Last sequence update)

(Rel. 42, Last annotation update)

(rophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
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                       Swiss Institute of Bioinfo
Bioinformatics Institute.
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AAA66725.1; -.
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                    entry is copyright. It is produced through a collaboration iss Institute of Bioinformatics and the EMBL outstation oinformatics Institute. There are no restrictions on its
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F -> S (IN REF. 1).

F -> L (IN REF. 1).
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ATP (BY SIMILARITY).
H-T-H MOTIF (BY SIMILARITY).
V->M: DEFECTIVE IN THE SYNTHESIS
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and are present before
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Matches 8
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HAMAP; MF 00209; -; 1.
InterPro; IPR008163; Inorg pphsph.
InterPro; IPR008162; Pyrophosphatase.
Pfam; PF00719; Pyrophosphatase; 1.
ProDom; PD002014; Inorg pphsph; 1.
PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-96135233; PubMed-8551578;
Marchigen N., Strauss J.H.;
"Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";
"Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";
J. Virol. 70:1173-1181(1996).
J. Virol. 70:1173-1181(1996).
-I- FUNCTION: May be involved in transcription termination by RNA
-I- FUNCTION: May be involved in transcription termination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LA AEDAL STANDARD; PRT; 383 AA.
Q26457;
Q26457;
G25-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La protein homolog (La ribonucleoprotein) (La protein albopictus (Forest day mosquito).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL445564; CAC13643.1; PIR; F90570; F90570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                              Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amounts are present in the cytoplasm.
-!- SIMILARITY: Contains 1 RNA recognition motif
-!- SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Nematocera; Culic NCBI_TaxID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                         PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                InterPro;
                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sindbis virus RNA replication. SUBCELLULAR LOCATION: Nuclear. Primarily nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymerase III. Binds RNA and minus strand of Sindbis virus
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                                                                                                                                                                                                                                         S80954; AAB35931.1; -
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DLDSKWLEEIKYFFSNY 127
                                                                                                                                                     IPR002344; Lupus_La.
IPR006630; Lupus_La_dom
IPR000504; RNA_rec_mot.
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MAGNESIUM 1 (BY SIMILARITY).

MAGNESIUM 1 AND 2 (BY SIMILARITY).

MAGNESIUM 1 (BY SIMILARITY).

; 65AFB1A06E3AAAD3 CRC64;
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(See http://www.isb-sib.ch/announce/
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L outstation -
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SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1. PROSITE; PS50102;

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RESULT 9
RPO2_VARV
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R InterPro; IPR007645; RNA_pol_Rpb2_3.

R InterPro; IPR007646; RNA_pol_Rpb2_4.

R InterPro; IPR007647; RNA_pol_Rpb2_5.

R InterPro; IPR007641; RNA_pol_Rpb2_6.

R InterPro; IPR007641; RNA_pol_Rpb2_7.

R InterPro; IPR007641; RNA_pol_Rpb2_7.

R Pfam; PF04565; RNA_pol_Rpb2_4; 1.

R Pfam; PF04566; RNA_pol_Rpb2_5; 1.

R Pfam; PF04567; RNA_pol_Rpb2_5; 1.

R Pfam; PF04567; RNA_pol_Rpb2_6; 1.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          P3981;
93981;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
DNA-directed RNA polymerase 132 kDa polypeptide
RPO132 OR A24R.
                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=India-1967 / Isolate Ind3;
MEDLINE=93202281; PubMed=8384129;
Shchelkunov S.N., Blinov V.M., Sandakhchiev
"Genes of variola and vaccinia viruses neces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
  -
                                                    protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-i-FUNCTION: DNA-dependent RNA polymerase catalyzes the transciof DNA into RNA using the four ribonucleoside triphosphates
                                                                                                                                                                                                                                                                                                                                                     Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                          Variola virus.
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EMBL; M35027; AAA48148.1; -.
PIR; H42519; RNVZ8T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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substrates.
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CATALYTIC ACTIVITY: N
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                                                                                                                                                                                                                                                                                                                         TaxID=10255;
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1164 AA;
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TY: Belongs to the RNA polymerase beta chain family.
  ACTIVITY:
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MW; B1F5C1484BA37D0D CRC64;
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Pred. No. 1.1;
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                                                                                   transcription
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                                                                                                                                                              the
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RESULT 10
V143_NPVAC
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Matches :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007645; RNA_pol_Rpb2_3.
InterPro; IPR007646; RNA_pol_Rpb2_4.
InterPro; IPR007647; RNA_pol_Rpb2_5.
InterPro; IPR007120; RNA_pol_Rpb2_5.
InterPro; IPR007120; RNA_pol_Rpb2_7.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF04566; RNA_pol_Rpb2_4; 1.
Pfam; PF04567; RNA_pol_Rpb2_4; 1.
Pfam; PF04567; RNA_pol_Rpb2_5; 1.
Pfam; PF04561; RNA_pol_Rpb2_6; 1.
Pfam; PF04561; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  V143 NPVAC
P24307;
                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992
01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a centre of the Ewiss Institute of Bioinformatics and the EWIST the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
                                                                                     "The complete DNA sequence
                                                                                                                                                                                                                                                                                                                                 Viruses;
                                                                                                                                                                                                                                                                                                                                             Autographa californica
                                                                                                                                                                                                                                                                                                                                                              P143.
                                                                                                                                                                                                                                                                                                                                                                           Helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X69198; CAA490
PIR; G36850; G36850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).

    -i- SUBUNIT: This enzyme consists of at least eight subunits.
    -i- SIMILARITY: Belongs to the RNA polymerase beta chain family.

                                                                                 polyhedrosis virus
                                                                                           MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., I
"The complete DNA sequence of Autographa californica
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                 "Nucleotide sequence of a gene essential for viral DNA replication the baculovirus Autographa californica nuclear polyhedrosis virus.' Virology 181:336-347(1991).
                                                                                                                                                                                                                                Lu A., Carstens E.B.;
                                                                                                                                                                                                                                            MEDLINE=91134998;
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                  Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; DNA-directed RNA polymerase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007121; RNA_pol_B
InterPro; IPR007645; RNA_pol_R;
InterPro; IPR007646; RNA_pol_R;
                                                                     irol
                        plogy 202:586-605(1994).

FUNCTION: Essential for the initiation of viral DNA replications such as controlling it may contribute to other functions such as controlling switch to the late phase and leading to the inhibition of
            protein synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503
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                                                                                                                                                                                                                                                                                                                                dsDNA viruses,
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(Rel.
(Rel.
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32,
35,
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Last
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            Required
                                                                                                                                                                                                                                                                                                                              nuclear polyhedrosis virus (AcMNPV)
, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
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Pred. No. 1.1;
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               for
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             very
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1164;
                                                                                                Possee R.D.;
muclear
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            gene
                                                       replication,
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RESULT 7
RPO2_COWPX
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Best Local S
Matches 13
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01-AUG-1990 (Rel
01-AUG-1990 (Rel
10-CCT-2003 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X67859; CAA48043.1; -.
PIR; JC1494; JC1494.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR00504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50102; RRM; 1. 1. PROSITE; PS00030; RRM RNP 1; 1. RNA-binding; Nuclear protein; PDOMAIN 111 187 RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cowpox virus (CPV).
Viruses; dsDNA viruses,
Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
DNA-directed RNA polymerase 132 kDa polypeptide (EC
                                                                            This
                                                                                                                                                                                                                                                                                                             polymerases."
J. Virol. 63:
                                                                                                                                                                                                                                                                                                                                                   STRAIN=Brighton red;
MEDLINE=89125698; PubMed=2915377;
Patel D.D., Pickup D.J.;
Patel D.D., Pickup D.J.;
"The second-largest subunit of the poxvirus RNA polymerase is similar
"The second-largest subunit of the poxvirus RNA polymerase is similar
                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPO132.
                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10243;
                                                                                                                                                                                                                                                                                                                                         the corresponding subunits of
                                                                                                       Comment=2 isoforms, 1/Late specific (shown here) and 2/Earl Late, are produced by alternative initiation. One transcriptional start site is operative at late times only the other is operative both at early and late times; SIMILARITY: Belongs to the RNA polymerase beta chain family.
                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                  (RNA)(N).
SUBUNIT: This enzyme consists
ALTERNATIVE PRODUCTS:
Event=Alternative initiation;
                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: N nucleoside
                                                                                                                                                                                                                                                                              FUNCTION: DNA-dependent RN of DNA into RNA using the
                                                                                                                                                                                                                                                                substrates.
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non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEAKICHQIEYYFGDF 28
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81.2%;
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                                                                                                                                                                                                                                                                                RNA polymerase catalyzes the transcription he four ribonucleoside triphosphates as
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   RNA-BINDING (RRM).
4; 033FD9CC1E475F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stage; Poxviridae; Chordopoxvirinae;
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R InterPro; IPR007121; RNA_pol_Rpb2_3.

R InterPro; IPR0071645; RNA_pol_Rpb2_4.

R InterPro; IPR007646; RNA_pol_Rpb2_5.

R InterPro; IPR007647; RNA_pol_Rpb2_5.

R InterPro; IPR007120; RNA_pol_Rpb2_5.

R InterPro; IPR007120; RNA_pol_Rpb2_7.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

R Pfam; PF04565; RNA_pol_Rpb2_4; 1.

R Pfam; PF04566; RNA_pol_Rpb2_5; 1.

R Pfam; PF04567; RNA_pol_Rpb2_6; 1.

R Pfam; PF04560; RNA_pol_Rpb2_7; 1.

R Pfam; PF04560; RNA_pol_Rpb2_8; 1.

R Pfam; PF04560; RNA_pol_Rpb2_8; 1.

R Pfam;
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Best Local (
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ZN FING
SEQUENCE
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P19798;
                                                                        Virology
[3]
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M26173; AAA42919.1; -. EMBL; M26173; AAA42920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
 STRAIN=Copenhagen;
Goebel S.J., Johns
Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                            Goebel
                                                                                                                                                               STRAIN=Copenhagen;
MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                    second-largest
polymerase.";
                                                                                                                                                                                                                                                                                                                          MEDLINE 91082452; PubMed=1824607; Amegadzie B.Y., Holmes M.H., Cole N.B.,
                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WR;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPO132 OR A24R.
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                                                       COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10254, 10249;
                                                                                                         The complete DNA
                                                                                                                                                                                                                                                                                         "Identification,
                                                                                                                                                                                                                                                                                                             SSON
                                                                                                                                                                                                    EQUENCE FROM N.A.
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                                                                                          179:
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1087 11
1164 AA;
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                                                                                          e DNA sequence
:247-266(1990)
                    Johnson
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1106
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                                                                                                                                                                                                                                                                          and expression of the vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
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POLYPEPTIDE, ISOFORM 1.
DNA-DIRECTED RNA POLYMERASE 13
POLYPEPTIDE, ISOFORM 2.
POR ISOFORM 2.
C4-TYPE (POTENTIAL).
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                    Perkus M.E.,
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Pred.
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                      Davis
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RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F. Bhat N.K.,

RX Albohins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Albohins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Albohins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Albohins R.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RX Brownstein M.J., Wachan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RX Rabas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Rabas S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Alborath S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,

RX Albey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RX Mhting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Mhting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Hollian M., Schmutz J., Myers R.M.,

RX Balakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RX RADAGERS S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

RX Thuman and mouse cDNA sequences.",

RX Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Best Local S
Matches 13
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01-OCT-1993 (Rel. :
01-OCT-1993 (Rel. :
15-MAR-2004 (Rel. :
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MOD RES
SEQUENCE
                                                                                                        SEQUENCE OF 1-11 FROM N.A.

Groelz D., Bachmann M.;

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor form
of RNA polymerase III transcripts including tRNA and 4.55, 55, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and reactivity of recombinant protein with poly(U) and human autoantibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Topfer F., Gordon T.,
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homolog)
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                        SUBUNIT: Interacts with DDX15 (By similarity) SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR SS-B.
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366
408 /
                                                                                         RNAB.
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. 43, Last annotation update)
homolog (La ribonucleoprotein)
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27,
43,
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T., McCluskey J.;
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Pred. No. 5.6e
1; Mismatches
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Sciurognathi; Muridae;
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5.6e-05;
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P38656;

01-FEB-1995 (Rel.

01-FEB-1995 (Rel.

28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM0360; KAN, 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS50030; RRM RNP 1; 1.

PROSITE; PS500030; RRM RNP 1; 1.

PROSPHOUSING (RRM).

RNA-BINDING (RRM).

111 187 RNA-BINDING (RRM).

2D75197692FDC933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSB OR SS-B.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                  Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC003820; AAH03820.1; -. EMBL; Y07951; CAA69249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L00993; AAA39415.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                   detection of
                                                                                                                                                                                                                                                                                                                                                                     Bachmann M.;
                                                                                                                                                                                                                                                                                                                                                                                        Semsei I.,
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93246255;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homolog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lupus La protein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus_La
InterPro; IPR006630; Lupus_La dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement
                                                                                                                                                                                                                                                                                                                                               Isolation
                                                                  PTM: Phosphorylated SIMILARITY: Contains
                                                                                                             SUBUNIT: Interacts with DDX15 SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                             polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 78,
                                                                                                                                                                                                                                                                        FUNCTION: La protein plays a role
                                                                                                                                                                                                                                                                                                lation of rat cDNA clones coding for the ction of species-specific variations."; 126:265-268(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
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                                                                                                                                                                                                                                                                                                                                                                                          Troester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD
                                                                orylated (By similarity).

Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                   PubMed=7916708;
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31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rat)
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Rodentia;
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81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
log (La ribonucleoprotein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76; DB 1;
Pred. No. 5.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                             (Probable).
                                                                                                                                   (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                          Schwemmle M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                          in the transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                          Igloi G.L.,
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                                                                                                                                                                                                                                                                                                                                  RA Strausberg R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.; Thuman and mouse cDNA sequences."; Thuman and mouse cDNA sequences."; Thuman and mouse cDNA sequences."; The proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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P05455;
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01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lupus La protein (i ribonucleoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta, and Skeletal muscle; MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89202037; PubMed=2468131; Chan E.K.L., Sullivan K.F., Tan E.M.; "Ribonucleoprotein SS-B/La belongs to
                             SEQUENCE OF 54-97 FROM N.A. MEDLINE=85166283; PubMed=3856888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89053970; PubMed=3192525;
Chambers J.C., Kenan D., Martin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences for RNA-binding.";
Nucleic Acids Res. 17:2233-2244(1989)
                                                                                                                                                                          "Characteristics
                                                                                                                                                                                                                                                               MEDLINE=88199081; PubMed=2452201;
                                                                                                                                                                                                                                                                                         SEQUENCE OF 54-408 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genomic structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                  140:3212-3218(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
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                                                                                                                                                                                                                                  Peterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD,
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (La autoantigen)
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81.2%;
                                                                                                                                                                       epitope mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Martin B.J., Keens amino acid sequence
                                                                                                                                                                                                                               M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76; 1
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               McNeilage L.J., Whittingham S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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5.5e-05;
2;
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                                                                                                                                                                                human autoantigen
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PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_
Systemic lupus erythematos
Nuclear protein

erythematosus;

_1; 1. sus; RNA-binding; Phosphorylation;

InterPro;
Pfam; PF05

InterPro;

InterPro; IPR002344; Lupus_La. InterPro; IPR006630; Lupus_La_dom.

IPR000504;

RNA_rec_mot

GO:0008334; P:histone mRNA metabolism; GO:0006400; P:tRNA modification; TAS.

C:ribonucleoprotein complex; F:mRNA binding; TAS. F:tRNA binding; TAS.

PRINTS;

; PR00302; LUPUSLA. SM00715; LA; 1. SM00360; RRM; 1.

rrm;

88888

GO:0000049; GO:0003729; MIM;

109090;

SSB.

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EMBL; X13697; CAA31985.1; --
EMBL; J04205; AAA51085.1; --
EMBL; BC001289; AAH01289.1; --
EMBL; BC020818; AAH02818.1; --
EMBL; BC020818; A31888.
                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del> <del>-</del> -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S Van Venrooij W.J., Pruijn G.J.M., "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, putative DEAH-box RNA helicase."; RNA 8:1428-1443(2002).

-!- FUNCTION: La protein plays a role in the transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Phosphorylation of the human La antigen on serine 366 car recycling of RNA polymerase III transcription complexes."; Cell 88:707-715(1997).
                                                                                                                                                                                                                                                                                                                                                                                   use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription termination by \overline{\text{RNA}} polymerase \overline{\text{EMBO}} J. 8:851-861(1989).
                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   :-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22346609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE=97207017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH DDX15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and 7-2 RNAs.
SUBURIT: Interacts with DDX15.
SUBCELLULAR LOCATION: Nuclear (Probable)
PTM: PHOSPHORYLATED. THE PHOSPHORYLATION
C-TERMINAL PART OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: Sera from patients with systemic often contain antibodies that react with t La protein as if this antigen was foreign.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.55, 55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TERMINAL PART OF THE PROTEIN.
PTM: The N-terminus is blocked.
                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the mammalian La protein: evidence for its tion termination by RNA polymerase III.";
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Usage
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366 can regulate
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rmal cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                     Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P28048;
01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
15-MAR-2004 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XENLA
                                                                                                                                                                                                                                                                                   This SWIS
           PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1
RNA-binding; Nuclear protein;
                                                                                                                      EMBL; X68817; CAA48715.1; -.
PIR; S33818; S33818.
InterPro; IPR002344; Lupus La_dom.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
RNA-binding; Nuclear protein; Phosphorylation.
DOMAIN 110 202 RNA-BINDING (RRM).
DOMAIN 315 331 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93287095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordat:
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homolog
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Lupus La protein homolog A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. Biol. 231:196-204(1993).

FUNCTION: La protein plays a role in the transcription of polymerase III. It is most probably a transcription term factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).

SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             erly D., Stutz
proteins from
                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBD outstation - European Bioinformatics Institute. There are no restrictions on its European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: There are two forms of La, LaA and LaB, in SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN. SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                         PTM: Phosphorylated (Probable). MISCELLANEOUS: There are two fo
                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly
                                                                                                                                                                                                                                                                                                                                                                                                   constant steady state level in mature oocytes,
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                                                                                                                                                                                                               an email to license@isb-sib.ch).
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315
427 AA;
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43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8510143;
F., Lin-Marq N., Clarkson S.G.;
Xenopus laevis. cDNA cloning an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Cranĭata; Vertebrata; l; Anura; Mesobatrachia; Pipoidea;
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annotation update)
(La ribonucleoprotein
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1.
; Phosphorylation.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a transcription termination
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RESULT 3
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P10881;
01-JUL-1989
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DOMAIN
SEQUENCE
                   SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; 1.
PROSITE; PS00030; RRM RNP 1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
RNA-binding; Nuclear protein; Phosphorylation.
RNA-BINDING (RRM)
DOMAIN 111 187 RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences for RNA-binding.",
Nucleic Acids Res. 17:2233-2244(1989).
Nucleic Acids Res. 17:2233-224 (1989).
-!- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor form
of RNA polymerase III transcripts including tRNA and 4.55, 55, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mámmalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The bear by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989
28-FEB-2003
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                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                  Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                    PIR; S03849;
                                                                                                                                                                                                                                                                                                                        EMBL; X13698; CAA31986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chan E.K.L., Sullivan K.F., Tan E.W
"Ribonucleoprotein SS-B/La belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89202037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pituitary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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                                                                                                                                                                                                                              InterPro; IPR000504;
                                                                                                                                                                                                                                                      InterPro; IPR006630;
                                                                                                                                                                                                                                                                            InterPro; IPR002344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELDULAR LOCATION: Nuclear (Probable).
PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES
C-TERMINAL PART OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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4EE30B5C262AD6A1
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Maximum Match 100%
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Maximum DB
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
   protein search, using
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129.452 Million cell updates/sec
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Gapop 10.0 ,
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  GenCore version (c) 1993 - 2004
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ETF2_MYXVL
ETF2_SFVKA
POLG_ECO1F
YC87_METJA
LAH1_SCHPO
Z277_HUMAN
Z406_HUMAN
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Compugen Ltd.
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   Q58683
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Q9q8k4
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6 mycoplasma
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6 drosophila
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XENIA STANDARD; PRT; 427 AA. 46; 46; 46; 46; 40; 406; 408; 404 (Rel. 43) Last sequence update) 8 La protein homolog B (La ribonucleoprotein B) (La autoantigen 10:40; 408; 404 (Rel. 43) Last annotation update) 8 La protein homolog B (La ribonucleoprotein B) (La autoantigen 10:40; 409; 401; 402; 403; 404; 404; 405; 404; 405; 405; 406; 406; 407; 407; 408; 409; 409; 409; 409; 409; 409; 409; 409	40 40.0 608 1 ALB2 SALSA 40 40.0 755 1 SEC6_RAT 40 40.0 756 1 SEC6 HUMAN 40 40.0 756 1 SEC6 HUMAN 40 40.0 756 1 SEC6 HUMAN 40 40.0 2911 1 FBNZ_HUMAN 39.5 39.5 297 1 YX01_CAEEL 39.5 39.5 859 1 STT_HUMAN 39.5 39.5 967 1 SYL_PYRHO 39.3 39.0 175 1 IPYR PSEPK 39.3 39.0 175 1 IPYR PSEPK 39.3 39.0 191 1 Y948_METJA 39.3 39.0 244 1 GRAK_HUMAN 39.3 39.0 254 1 HEM6_VIBCH 39 39.0 305 1 HEM6_VIBCH ALIGNWENTS ALIGNWENTS
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hypothetical protein MYPU 4700 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90570
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: F90570
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <KUR>
A;Cross-references: GB:AL445566; PID:g14089884; PIDN:CAC13643.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
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F90570
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C;Superfamily: AcMNPV helicase
C;Keywords: ATP; DNA binding; DNA repair; DNA replication; hydrolase; nucleotide binding F;917-924/Region: nucleotide-binding motif A (P-loop)
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A;Molecule type: DNA
A;Residues: 1-125', F', 127-1148,', F', 1150-1221 <AYR>
A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66725.1; PID:g559164
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Search completed: September 10, 2004, 18:02:33 Job time : 16.0782 secs
                                                                                                                                                                                                                                                              C; Superfamily: inorganic pyrophosphatase
                                                                                                                                            Query Match
Best Local Similarity 47...
"...ches 8; Conservative
                                                                                                                                                                                                                                                                                    Gene: MYPU 4700
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Local Similarity 61.5%;
hes .8; Conservative
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111 DLDSKWLEEIKYFFSNY 127
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6; Mismatches
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Pred. No. 6
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RESULT 11
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A;Reference number: A4253; MUID:91021027; PMID:2219722
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
C;Keywords: leucine zipper; nucleotidyltransferase; transcription; zinc finger
F;1087-1106/Region: leucine zipper motif
F;1087-1106/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions characterize number: Z20488; MUID:94088747; PMID:8264798
A;Accession: T28566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-directed RNA polymerase (EC 2.7.7.6) 133K chain - variola major virus C;Species: variola major virus C;Decies: variola major virus C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000 C;Accession: T28566
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C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
C;Keywords: nucleotidyltransferase; transcription; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1164 <PAT>
A; Cross-references: GB: M26173; NID: g323393;
A; Cross-references: CD: M26173; NID: g323393;
A; Cross-references: GB: M26173; NID: g323393;
A; M26173; NID: g32339;
A; M27375;
A; M27375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Patel, D.D.; Pickup, D.J.
J. Virol. 63, 1076-1086, 1989
A;Title: The second-largest subunit of the A;Reference number: A31879; MUID:89125698;
A;Accession: A31879
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                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60876.1; A;Experimental source: strain Bangladesh-1975 C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-1164 <MAS>
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Pred. No.
                                                                                                                                                     Score 53;
Pred. No.
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Pred. No.
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                                                                                                                                                                                  DB 2;
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A;Title: Nucleotide sequence of a gene essential for viral A;Reference number: A38499; MUID:91134998; PMID:1994581 A;Accession: A38499
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G36850
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C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
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                                                       A;Molecule type: DNA
A;Residues: 1-1221 <LUA>
A;Cross-references: EMBL:M57687
                                                                                                                                                                                                                  C; Accession: A38499; H72861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: DNA-directed RNA polymerase 132K polypeptide
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A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49069.1; PID:g297307
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A; Accession: G36850
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A;Cross-references: GB:X16780; NID:g5830555; PIDN:CAB54728.1;
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A;Molecule type: DNA
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                                       R;Ayres,
                                                                                                                                                                             Virology 181, 336-347, 1991
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Best Local Similarity
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M.D.; Howard, S.C.; Kuzio, 202, 586-605, 1994
The complete DNA sequence
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Pred. No. 3.1;
  of.
                                       J.; Lopez-Ferber, M.; Possee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Autographa californica nuclear polyhedrosis virus.
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Gene 126, 265-268, 1993
A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection A;Reference number: JC1494; MUID:93246255; PMID:7916708
                                                                                                                     R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                    capsular polysaccharide synthesis enzyme Cap5P [imported] - Staphylococcus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Sammons, L.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, August A;Description: The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ay act as a transcription termination factor.

C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat

C;Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: liver C; Comment: This protein associates with a variety of small RNA molecules,
                                       C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89777
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A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C44E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
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Best Local S
Matches 13
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;151-158/Region: RNA-binding RNP1 motif
;227-415/Domain: phosphorylated #status
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Introns: 45/1; 114/3
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source: strain Bristol N2; clone C44E4
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Pred. No.
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Pred. No.
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C;Genetics:
A;Gene: capP
C;Superfamily: lipopolysaccharide biosynthesis protein bplD
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A;Accession: H42519
A;Molecule type: DNA
A;Residues: 1-1164 <GOE>
A;Cross references: GB:M35027; NID:g335317; PIDN:AAA48148.1; PID:g335496
A;Experimental source: strain Copenhagen
R;Amegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss,
R;Arnegadzie, B.Y.; Holmes, M.H.; Moss,
R
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C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991
C;Accession: H42519; A38517
R;Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, Virology 179, 517-563, 1990
A;Tille: Appendix to "The complete DNA sequence of DNA sequence 
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                                                                                                                                   A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1164 <AME>
A;Residues: 1-1164 <AME>
A;Cross-references: EMBL:M37415; NID:g335800; PIDN:AAA72882.1; PID:g335801
A;Experimental source: strain WR
A;Experimental source: strain WR
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C;Superfamily: DNA-directed RNA polymerase 132K polypeptide
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A;Variety: strain Ankara
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A; Residues: 1-1156 < ANT>
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Best Local Similarity
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3.J.; --
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                                                         Johnson, G.P.;
47-266, 1990
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58.8%; Pred. No. 3
                                                                                                   Perkus,
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Pred. No. 0.68;
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                                                                                                         S.W.;
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                                                                                                         Winslow,
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                                                                                                              J.P.; Paoletti,
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A;Molecule type: mRNA
A;Residues: 1-408 <CHA>
A;Residues: GB::04205; NID::g178686; PIDN::AAA51885.1; PID::g178687
A;Cross-references: GB::04205; NID::g178686; PIDN::AAA51885.1; PID::g178687
R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with constant Reference number: S03848; MUID::89202037; PMID::2468131
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C;Species: Homo sapiens (man)

C;Date: 21-May-1990 #sequence revision 26-May-1994 #text change 22-Jun-1999

C;Accession: A31888; S03848; Ā22956; A61051; S11013; I55553; I70205; I70206; A31273

R;Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.

J. Biol. Chem. 263, 18043-18051, 1988

A;Title: Genomic structure and amino acid sequence domains of the human La autoantigen.

A:Reference number: A31888; MUID:89053970; PMID:3192525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology C;Keywords: blocked amino end; phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology <RRM>F;113-118/Region: RNA-binding RNP2 motif F;151-158/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Note: part of this sequence was confirmed by protein sequencing C;Comment: This protein associates with a variety of small RNA molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus A;Reference number: S03848; MUID:89202037; PMID:2468131
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F;113-118/Region:
F;151-158/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonucleoprotein La - human
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome
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C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change
                                                                         A; Molecule type: mRNA
A; Residues: 1-408 < CH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-404 < CHA>
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                                            A;Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1; PID:g36415
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Keene, J.
Sci. U.S.
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94.1%;
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81.2%;
  82, 2115-2119,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiger
                                                                      N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-C;Species: Rattus norvegicus (Norway rat)
                       C; Date: 24-Feb-1994 #sequence_revision C; Accession: JC1494; S25145
                                                                                                                        ribonucleoprotein La -
                                                                                                                                                       JC1494
                                                                                                                                                                            RESULT 5
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A;Molecule type: mRNA
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457
R;Kohsaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka,
J. Clin. Invest. 85, 1566-1574, 1990
A;Title: Fine epitope mapping the human SS-B/La protein: Identification of A;Reference number: I5553; MUID:90237237; PMID:1692037
A;Accession: I5553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Sturgess, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, R. J. Immunol. 140, 3212-3218, 1988
A;Title: Characteristics and epitope mapping of a cloned human autoantigen La. A;Reference number: S11013; MUID:88199081; PMID:2452201
A;Accession: S11013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. Lett. 2ž, 65-72, 1989
A;Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
A;Reference number: A61051; MUID:89379261; PMID:2476379
                                                                                                                                                                                                                                        F;228-408/Domain:
                                                                                                                                                                                                                                                                    F;113-118/Region: F;151-158/Region:
                                                                                                                                                                                                                                                                                                                               F;112-178/Domain:
                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2 C; Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:SSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 279-342 <RE3>
A;Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
C;Comment: This protein associates with a variety of small RNA molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M35263; NID:g338492;
A;Accession: I70206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 174-224 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 81-107 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: this sequence has been revised in reference R;Nyman, U.; Ringertz, N.R.; Pettersson, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 45-97, 'LK' <CH3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: A22956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Isolation and analysis of cDNA clones expressing human lupus La antigen. A;Reference number: A22956; MUID:85166283; PMID:3856888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:125359; OMIM:109090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Molecule type: mRNA
                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                        Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: I70205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:M35261; NID:g338491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: GB:J04205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     act as a transcription termination factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translated from GB/EMBL/DDBJ
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                                                                                                                     13;
                                                          w
                                                                                                                                              Similarity
                                                       LDTKICEQIEYYFGDF 18
LEAKICHQIEYYFGDF 28
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                                                                                                                     Conservative
                                                                                                                                                                                                                                     phosphorylated #status experimental
                                                                                                                                                                                                                                                                 RNA-binding RNP2 motif RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                            ribonucleoprotein repeat homology
                                                                                                                                           76.0%;
81.2%;
                                                                                                                  Score 76; DB
Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAA36653.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAA36652.1; PID:g338495
                                                                                                                                                 0.0002;
                                                                                                                                                                                DB 1;
                                                                                                                                                                          Length 408;
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                                                                                                                     Gaps
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Bartsch, H.; Schwemmle,

26-May-1994

#text_change

22-Jun-1999

M.; Igloi, G.L.; Bachmann,

Title:
Perfect score:
Sequence: US-09-836-073-15 100 1 LDLDTKICEQIEYYFGDF 18

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283366

283366 seqs, 96191526 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

220 220 220 220 220 220 220 220 220 220	Result
4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	Score
888.0 76.0 76.0 76.0 76.0 76.0 76.0 53.0 53.0 53.0 53.0 53.0 53.0 53.0 53	. I co
428 428 404 404 415 396 396 396 3164 1164 1164 1164 1164 1164 1164 116	
111110001100010000100011111	ag .
S33814 S33849 A31888 JC1494 JC1494 JC17977 T37971 T3741 RNVZCP T28566 F72166 F72166 F72166 F72166 F721670 F90570 F90570 F40570 F90570 F40577 F90570 F40577 F90570 F40577 F90570 F40577 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F90570 F	ib
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298	298	260	199	63	140	1055	421	277	270	199	788	759	658	505	366
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	2
T43542	T38937	H71979	B97180	C96942	C96957	AD2499	AE2473	AD0121	F64460	AI1512	A71076	AC0368	D96656	B90181	JQ0513
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ALIGNMENTS

RESULT 2 S33818 S33818 N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Xenopus laevis (African clawed frog) C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-199 C;Accession: S33818; S28545 R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G. J, Mol. Biol. 231, 196-204, 1993 A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental e. A;Reference number: S33817; MUID:93287095; PMID:8510143 A;Residues: 1-428 <sch> A;Accession: S33818 A;Accession: S33818 A;Accessidues: 1-428 <sch> A;Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874 C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: phosphoprotein; RNA binding</sch></sch>	Query Match 94.0%; Score 94; DB 1; Length 427; Best Local Similarity 100.0%; Pred. No. 2.7e-07; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 LDLDTKICEQIEYYFGD 17 Db 10 LDLDTKICEQIEYYFGD 26	A; McCessium. A; McCessium. A; Residues: 1-427 <sch> A; Residues: 1-427 <sch> A; Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876 A; Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876 C; Comment: This protein associates with a variety of small RNA molecules, to ay act as a transcription termination factor. C; Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C; Keywords: phosphoprotein; RNA binding F; 111-117/Domain: ribonucleoprotein repeat homology <rrm> F; 112-117/Region: RNA-binding RNP2 motif F; 150-157/Region: RNA-binding RNP1 motif F; 227-427/Domain: phosphorylated #status predicted <phy></phy></rrm></sch></sch>	a.B - African clawed frog autoantigen:SS-B/La; ribonucleoprotein SS-B laevis (African clawed frog) #sequence_revision 26-May-1994 #text_change 22-Jun-19; \$28544 z, F:; Lin-Marq, N.; Clarkson, S.G. 196-204, 1993 s from Xenopus laevis. cDNA cloning and developmental \$33817; MUID:93287095; PMID:8510143
tt_change 22-Jun-1999 and developmental expression. PID:g64874 all RNA molecules, most of which repeat homology		D:g64876 colecules, most of which mology	22-Jun-1999 .opmental expression.

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OA4678
ID OA467
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Matches 11
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C14C6.12.
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044678;
01-JUN-1998
01-OCT-2003
01-OCT-2003
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InterPro; IPR006630; Lupus_La_dom.
Pfam; PF05383; La; 1.
SMART; SM00684; DM15; 3.
SMART; SM00715; LA; 1.
SMART; SM00715; LA; 1.
SEQUENCE 928 AA; 103745 MW; 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone:P0499C11.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001080; BAA90356.1; -.
Gramene; Q9LJ02; -.
InterPro; IPR006607; DUF DM15.
SEQUENCE FROM N.A.
STRAIN-Bristol N2;
Wilson R.;
Wilson R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ
EMBL; AF039051; AAB94258.2; -
Hypothetical protein.
SEQUENCE 91 AA; 10407 MW; D16D2BD4011F8762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                   Waterston R.;
Submitted (AP)
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                David M., Wohldmann P., Bauer C., Antoniou B.;
"The sequence of C. elegans cosmid C14C6.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to KIAA0731 protein.
Oryza sativa (Rice).
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| LRAKILTQVEYYFSGD 293
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Pred. No. 25;
1; Mismatches
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     D16D2BD4011F8762 CRC64;
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KICNVIEYMTGDF 18
            KICHQIEYYFGDF 18
                          Conservative
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Pred. No. 3;
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Search completed: September 10, 2004, 18:00:07 Job time: 42.229 secs

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RESULT 12
Q99X5
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SEQUENCE FROM N.A.

STRAIN=Reynolds and Newman;

STRAIN=STRAIN=Reynolds and Newman;

MEDLINE=97388567; PubMede9245821;

MEDLINE=97388567; PubMede9245821;

Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.;

Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.;

"The Staphylococcus aureus allelic genetic loci for serotype 5

"The Staphylococcus aureus allelic genetic genes flanked by one of the stape of 
                                                                                                                                                                                                                                                                        Q99X57;
01-JUN-2001
01-JUN-2001
01-JUN-2003
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TIGRFAMs;
SEQUENCE
                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Capsular polysaccharide synthesis enzyme Cap5P.
CAPP OR SAV0164 OR SA0159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U81973; AAC46099.1; -.
HSSP; P27828; 1FGD.
GO: GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;
GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Reynolds and Newman;
MEDLINE=98125727; PubMed=9466251;
Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S.,
"Identification of a gene essential for O-acetylation of staphylococcus aureus type 5 capsular polysaccharide.";
Mol. Microbiol. 27:9-21(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Staphylococcus aureus cap50 and cap5P genes functionally complement mutations affecting enterobacterial common-antigen biosynthesis in Escherichia coli.";
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STRAIN=Reynolds and Newman;
MEDLINE=98101481; PubMed=9440531;
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Bacteria; Firmicutes; Bacillales;
                                                                                                                                              Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Bagga N., Wann E.R., Foster T.J., Lee J.C.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ
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                      SPECIES=S.aureus (strain Mu50), an MEDLINE=21311952; PubMed=11418146;
                                                                                                                       Bacteria; Firmicutes;
NCBI_TaxID=158878, 158
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                                                                            SEQUENCE FROM N.A.
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Pfam; PF02350; Epimerase_2; 1.
TIGRPAMS; TIGR00236; wecB; 1.
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  Ohta T.,
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llarity 72.7%;
Conservative
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44328 MW;
     Uchiyama
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Pred. No. 8.7;
1; Mismatches
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     Kobayashi
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Q8LMP9;
01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C.
Saski C., Henry D., Oates R.,
"Rice Genomic Sequence.",
"Rice Genomic Sequence.",
Submitted (JUN-2002) to the EN
                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. OSJNBA0011L14.12.
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TIGRFAMs; TIGR00236; wecB; 1.
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EMBL; AP003358; BAB56326.1;
EMBL; AP003129; BAB41379.1;
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                                                                                                                                                                          Hypothetical protein SEQUENCE 481 AA; '
                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
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InterPro; IPR00630; Lupus_La dom.
InterPro; IPR00630; Lupus_La dom.
InterPro; IPR0060504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00380; La; 1.
PFNNTS; PR00300; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ
EMBL; AY050403; AAK91419.1; -
EMBL; BT000588; AAN18157.1; -
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
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                  Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants
acquired MRSA.";
Lancet 359:1819-1827(2002).
                                                                                                                         Baba T., Takeuchi
Nagai Y., Iwama N
                                                                                                                                                                                                                                                                           Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                          Capsular polysaccharide CAPSP OR MW0139.
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01-OCT-2002
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                                                                                                                                                                               MEDLINE=22040717;
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       AP004822; BAB94004.1;
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                                                                                                                      2040717; PubMed=12044378;
Takeuchi F., Kuroda M., Yuzawa
Twama N., Asano K., Naimi T.,
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Bacillales;
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                                                                          high virulence community-
                                                                                                                         H., Aoki K.-I.,
Kuroda H., Cui
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RESULT 11
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ID P7238
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P72382;
01-FEB-1997
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"Molecular characterization and transcriptional analysis of type
"Molecular characterization and transcriptional analysis of type
"Bacteriol in Staphylococcus aureus.";
J. Bacteriol 179:1614-1621(1997)
EMBL; U73374; AAB49445.1; -.
EMBL; U73374; AAB49445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003331; Epimerase_2.
Pfam; PF02350; Epimerase_2; 1.
TIGRFAMs; TIGR00236; wecB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96178981; PubMed=86
Sau S., Lee C.Y.;
"Cloning of type 8 capsule
production of different cap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus Bacteria; Firmicutes;
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TIGRFAMs; TIGR00236; wecB; 1
Complete proteome.
SEQUENCE 381 AA; 43106 MW
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01-JUN-2003
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8; Conserv
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8; Conserv
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391 AA; 44247 MW;
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Pred. No. 8.7;
L; Mismatches
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P95709; P95709; 01-MAY-1997 01-MAY-1997 01-JUN-2003

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Q8T8V5;
01-JUN-2002
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               FlyBase; FBgn0011638; La.
GO; GO:0008098; F:5S rRNA primary t
GO; GO:0003723; F:RNA binding; NAS.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
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PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 401 AA; 46138 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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LA OR CG10922.
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PRINTS; PR00302; LUE
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                                                                                                                                                                Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; AY075257; AAL68124.1; -.
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Celniker S.;
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73.3%;
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Last annotation updat
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                                                                                                                       transcript binding; IDA
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PRINTS; PR00302; LUPUSLA.
SWART; SW00715; LA; 1.
SMART; SW00760; RRM; 1.
PROSITE; PS50100; RRM; 1.
PROSITE; PS50030; RRM RNP 1; 1.
SEQUENCE 390 AA; 44869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similarity to RNA-binding protein.
Arabidopsis thaliana (Mouse-ear cress).
Enkaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidonaia
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Q9FL36;
01-MAR-2001
                   O94A38 PRELIMINARY; PRT; 4;
O94A38; PRELIMINARY; PRT; 4;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last seque)
O1-OCT-2003 (TrEMBLrel. 25, Last annot;
AT5946250/MPIJ2 3,
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB010698; BAB11080.1; -. GO; GO:0005634; C:nucleus; IEA. GO; GO:0003723; F:RNA binding; IEA. InterPro; IPR002344; Lupus La. InterPro; IPR006630; Lupus La_dom. InterPro; IPR000504; RNA_rec_mot.
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STRAIN-Columbia;
MEDLINE-98344145; PubMed-9679202;
MCDLINE-98344145; PubMed-9679202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome features of the regions of 1,381,565 bp covered by twent physically assigned P1 and TAC clones.";
DNA Res. 5:131-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Viridiplantae;
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  Streptophyta;
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Last annotation updat
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    Embryophyta; Tracheophyta;
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MGD; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR005234; Lupus La.
InterPro; IPR006630; Lupus La dom.
InterPro; IPR006630; Lupus La dom.
InterPro; IPR00564; RNA_rec_mot.
Pfam; PF0338; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM; RNP_
  Q7ZTK2;
Q7ZTK2;
01-JUN-2003
01-JUN-2003
01-OCT-2003
Similar to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1. PR101TS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SEQUENCE 381 AA; 43891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
5jogren syndrome antigen B.
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STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8BTU4;
01-MAR-2003
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot
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17; Conserv
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PS00030; RRM_RNP_1; 1.
415 AA; 47657_MW;
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3 (TrEMBLrel. 24,
3 (TrEMBLrel. 24,
3 (TrEMBLrel. 25,
lupus LA protein
                                                                                                                                                                                                                                                                                                                       Conservative
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homolog B.
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                                                                                                                                                                                                                                                                                                                                            Score 95;
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Pred. No.
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                                                                                                                   PRT;
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2.4e-07;
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2.2e-07;
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Best Local S
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                                                                                                                                                                                                  L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMBL/GenB
EMBL; Ara467897; AAL76269 1;
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La.
InterPro; IPR006630; Lupus La.
InterPro; IPR006630; RNA_rec_mot.
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OLJUN-2002 (Trembirel. 21, Created)

OLJUN-2002 (Trembirel. 21, Last sequence update)

OL-OCT-2003 (Trembirel. 25, Last annotation updat

Theranslated region binding-protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC046654; AAH46654.1; -. GO; GO:0005634; C:nucleus; IEA. GO; GO:0003723; F:RNA binding; IEA. InterPro; IPR002344; Lupus_La. InterPro; IPR002344; Lupus_La. dom. InterPro; IPR006630; Lupus_La. dom. InterPro; IPR000504; RNA_rec_mot. Pfam; PF00076; rrm; 1.
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 1.
SEQUENCE 427 AA; 48996 |
                                                                                                 PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                        PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                            Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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Submitted (FEB-2003) to the
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae;
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13
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                                                 l Similarity
12; Conserv
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12; Conserv
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PS00030; RRM RNP_1; :
206 AA; 23992 MW;
                        LEAKICHQIEYYFGD 17
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Veognathae; Galliformes; Phasianidae; Phasiani
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80.0%;
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80.0%;
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  27
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                                                Score 69; DB 13;
Pred. No. 0.0023;
2; Mismatches
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Pred. No. 0.0033;
1; Mismatches
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                                                                                                     965B62F7DFFB90E9 CRC64;
                                                                            DB 13; Length 206;
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Tisting first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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137.751 Million cell updates/sec
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99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                  sp_organelle:*
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sp plant:*
sp rodent:*
sp virus:*
sp vertebrate:*
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sp bacteriap:*
sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	σ	σ	4	ω	N	Ľ	Result No.
48	48	48.5	49	49	49	49	49	50	50	51	62	69	70	95	95	Score
48.5	48.5	49.0	49.5	49.5	49.5	49.5	49.5	50.5	50.5	51.5	62.6	69.7	70.7	96.0	96.0	Query Match Length DB
545	91	928	481	391	391	391	381	422	411	390	401	206	427	415	381	ength
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080567	044678	Q9LJ02	Q8LMP9	Q99X57	P95709	P72382	8NYN8	Q94A38	Q9FL36	Q8T8V5	Q7ZTI0	Q8QHI5	Q7ZTK2	Q8BTU4	Q9СҮВ9	ID
O80567 arabidopsis	044678 caenorhabdi	Q91j02 oryza sativ	Q81mp9 oryza sativ	Q99x57 staphylococ	P95709 staphylococ	P72382 staphylococ	Q8nyn8 staphylococ	Q94a38 arabidopsis	Q9fl36 arabidopsis	Q8t8v5 drosophila	Q7zti0 brachydanio		Q7ztk2 xenopus lae	Q8btu4 mus musculu	Q9cyb9 mus musculu	Description

	 45	44	4.	42	41	40	9	3 8 8	37	36	35	<u>ب</u>	(s) (s)	.: .:	ω H	ယ ပ	29	28	27	26	25	24	23	22	21	20	19	18	17
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	42.4	42.4	42.4	42.9	42.9	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.4	43.9	44.4	44.4	44.9	45.5	46.5	47.5	47.5	47.5
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MENTS	Q88ya5 lactobacill	Q7vial helicobacte	-	bacteroi	Q97db6 clostridium	ב		Q86pr0 cryptospori	0	Q18215 caenorhabdi				0		Q83bp5 coxiella bu			O80788 arabidopsis		OS8603 pyrococcus		ູເດ	റ		VIBTIO	Q7xvc6 oryza saciv	001806 caenorhabdi	Q9zp89 neurotheca

ALIGNMENTS

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Wynshaw-Boris A., Hayashizaki Y., "Functional annota Nature 409:685-690 EMBL; AKO17822; BA MGD; MGI:98423; Ss	Nordone P., Ring B., Sasaki H., Sato K., (Suzuki H., Toyo-oka)	Brownstein M.J., Bult Gustincich S., Hill D. Lyons P., Marchionni I	Sakai K., Oki Blake J., Bof	· a	Saito T., Ok Kadota K., M	Aizawa K., I	Kawai J., Sh Arakawa T.,	STRAIN=C57BL MEDLINE=2108	SEQUENCE FRO	NCBI_TaxID=10090;	Mammalia; Eutheria;	Mus musculus (Mouse)	Sjogren syndrome SSB.	01-OCT-2003	01-JUN-2001	09CYB9
otat 690() BAB SSb	スいっ		II. D. Okido T., Furuno M., Aono H., Baldarelli R., J., Boffelli D., Bojunga N., Carninci P., de Bona	n W., Gaasterland T., Gissi C., King B., Nochiwa n., Lewis S., Matsuc Y., Nikaido II., Pesole G., Quackenbush Marmar I. Washio	Saito T., Okazaki Y., Gojobori T., Bono H., Kabukaw Kadota K., Matsuda H.A., Ashburner M., Batalov S.,	Izawa M., Nishi K.,	Kawai J., Shinagawa A., Shibata K., Arakawa T., Hara A., Fukunishi Y.,	STRAIN=C57BL/60; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851;	FROM N.A.	0090;	theria; Rodentia;		rome antigen B.	(TrEMBLiel. 25,		PRELIMINARY;
Hasegawa 11-lengt	, Ringwald M., Rodriguez Schoenbach C., Seya T., K., Wang K.H., Weitz C.	Tetcher C., mann M., Hu shima J., M	M., Aono H. Inga N., Car	Y., Nikaido	hburner M.,	o					a; Sciurognathi;			Last annotati	Œ	PRT; 3
., Kawaji F mouse cDNA	C.,	., Fletcher C., Fujita M., Gariboidi M., ., Hofmann M., Hume D.A., Kamiya M., Lee N L., Mashima J., Mazzarelli J., Mombaerts F	Furuno M., Aono H., Baldarelli R., Barsh G D., Bojunga N., Carninci P., de Bonaldo M.F	I., Pesole G.	M., Batalov S., Ca	H., Kondo S	Yoshino M., Itoh Konno H., Adachi J	ŀ			Muridae;	Tout obvoto.		annotation update)		381 AA.
Kohts lecti	I., Sakamoto N., Shibata Y., Storch KF., Whittaker C., Wilming L.,	M., Gariboidi M., Kamiya M., Lee N.H., i J., Mombaerts P.,	Barsh G., ldo M.F.,	34	Casavant T.,	Yamanaka	M., ISDII				Murinae; Mus.					

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hypothetical protein C54G10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20230
R;Matthews, L.
submitthed to the EMBL Data Library, June 1996
A;Reference number: Z19240
A;Accession: T20230
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-568 <HEI>
A;Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; PIDN:AAF96979.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                       A; Status: Preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-839 <WIL>
A; Cross-references: EMBL: Z75532; PIDN: CAA99812.1; GSPDB: GN00023; CESP:C54G10.2
A; Experimental source: clone C54G10
C; Genetics:
C; Genetics:
C; Genetics:
A; Gene: CESP:C54G10.2
A; Gene: CESP:C54G10.2
A; Map position: 5
A; Introns: 12/1; 34/3; 69/3; 326/1; 432/3; 535/3; 668/2
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C;Superfamily: response regulator, Hnr type; response regulator homology
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Apr-2003
C;Accession: C82379
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Search completed: September 10, 2004, 18:02:31 Job time: 15.0782 secs
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                                                                                                              LEAKIGELSGSHQIEQFFG
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A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A;Reference number: Z14180
A;Accession: T00677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nypothetical protein At2g43970 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein F6213.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00677; G84872
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T00677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C44E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-529 <STO>
A;Cross-references: GB:AE002093; NID:g3212854; PIDN:AAC23405.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: G84872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
A; Gene: F6E13.10; At2g43970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                          A; Experimental source: strain Bristol N2; clone C44E4
                                                                                                                                                                                                                                                                                                                                A;Residues: 1-396 <SAM>
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T30953
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                                                                                                                                                                                     Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                   Map position: I
                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:AF003140; PIDN:AAB54169.1
                                                                                                        Matches
                                                                                                                                                                                                          Introns: 45/1; 114/3
Note: C44E4.4
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8; Conserv
                       DOKIIKOLEYYFGN
                                                                EAKICHQIEYYFGD 17
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                                                                                                        Conservative
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66.7%;
                                                                                                                       47.5%;
57.1%;
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                                                                                                    Score 47; DB Pred. No. 4.9; 3; Mismatches
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Pred. No. 4.5;
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                       RESULT 14
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response regulator VCA1086 [imported] - Vibrio cholerae
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
C;Accession: T39937
                                                                                                                                                                                                                                                                           A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-298 <UTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: The La protein in Schizosaccharomyces pombe: a A;Reference number: Z22560; MUID:98067398; PMID:9404894 A;Accession: T43542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Badcock, K.; Churcher, C.M.; Wood, V.; Barre submitted to the EMBL Data Library, April 1997
                                                                                                                                                      A; Description: the binding of the La protein to tRNA precursors C; Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                C; Function:
                                                                                                                                                                                                                     A;Gene: sla1
                                                                                                                                                                                                                                                                                                                                                      A; Description: Screening of A; Reference number: Z22428
                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, E A; Description: Screening of S. pombe
                                                                                                                                                                                                                                                                                                                                                                                                                         R;Utsumi,
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-298 <VAN>
A;Cross-references: EMBL:AF022949; PIDN:AAB82145.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Van Horn, D.J.; Yoo, C.J.; Xue, D.; Shi, H.; Wolin, RNA 3, 1434-1443, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000 C;Accession: T43542; T43325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-binding protein La1 homolog - fission yeast (Schizosaccharomyces N;Alternate names: La autoantigen; ribonucleoprotein La homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
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A; Residues: 1-298 <BAD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rna binding protein - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                          A; Accession: T43325
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Best Local
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                                                                           Similarity 7; Conserv
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EAEVLKOVEFYFSD 77
                                   EAKICHQIEYYFGD 17
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                                                                             Conservative
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Pred. No.
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Pred. No. 5.5;
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e cDNA library using
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R;Bai, C.; Li, Z.; Tolias, P.P.
Mol. Cell. Biol. 14, 5123-5129, 1994
A;Title: Developmental characterization of a Drosophila RNA-binding protein homologous
A;Reference number: A53773; MUID:94309632; PMID:8035794
A;Accession: A53773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874 C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Scherly, D.;
J. Mol. Biol '
                                                                                                                        C;Species: Drosophila melanogaster
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
C;Accession: A53781
R;YOO, C.J.; Wolin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae:
A;Reference number: A53781; MUID:94309661; PMID:8035818
A;Accession: A53781
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A53773
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A;Tille: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           La/SS-B homolog D-la - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: leucine zipper; RNA binding
               A;Cross-references: GB:L32988; NID:g488469; PID:g488470 C;Genetics:
                                                           A; Molecule type: mRNA
A; Residues: 1-390 < YO
                                                                                                                                                                                                                                                                                 ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
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C;Genetics:
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A; Residues: 1-390 <BAI>
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A;Gene: FlyBase:La
                                                                                                        A;Status: preliminary
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Best Local S
Matches 9
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Best Local Similarity
Matches 11; Conser
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                                                           1-390 < 400>
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78.6%;
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Pred. No.
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Pred. No.
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81

KICNVIEYMTGDF KICHQIEYYFGDF 18

93

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A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capsular polysaccharide synthesis enzyme Cap5P [imported] - Staphylococcus aureus
C;Spscles: Staphylococcus aureus
C;Dats: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89777
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H89777
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                                                                                                                                                                                                                                                    R;David, M.; Wohldmann, P.; Bauer, C.; Antoniou, l
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid (
A;Reference number: Z21210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: capP
C;Superfamily: lipopolysaccharide biosynthesis protein bplD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Whole genome sequencing of metricillin-resistant Stapylococcus A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: H89777
                                                                                                                                                                                                                                                                                                                  C; Accession: T32701
R; David, M.; Wohldmann,
                                                                                                                                                                                                                                                                                                                                                     hypothetical protein C14C6.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change
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A;Experimental source: strain N315
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A; Residues: 1-391 < KUR>
                                                                                                                                             A;Cross-references: EMBL:AF039051; PIDN:AAB94258.1; GSPDB:GN00023; CESP:C14C6.12
A;Experimental source: strain Bristol N2; clone C14C6
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-166 < DAV>
                                                                       A; Introns:
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Best Local
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72.7%;
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Score 48; DB
Pred. No. 1.4;
1; Mismatches
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Pred. No.
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Pred. No.
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1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-19, 'E', 21-47 < NYM'
R; Sturgess A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, R.
J. Immunol. 140, 3212-3218, 1988
J. Title: Characteristics and epitope mapping of a cloned human autoantigen La.
A; Reference number: S11013; MUID:88199081; PMID:2452201
A; Accession: S11013
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
A;Reference number: A22956; MUID:85166283; PMID:3856888
A;Accession: A22956
                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2 C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 279-342 <RE3>
A;Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
C;Comment: This protein associates with a variety of small RNA molecules,
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A; Residues: 'E',55-287,'V',289-408 <STU>
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A; Molecule type: mRNA
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A;Accession: S03848
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A;Residues: 45-97,'LK' <CH3>
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;Residues: 174-224 <RE2>
;Cross-references: GB:M35263; NID:g338492; PIDN:AAA36653.1; PID:g338496
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;Residues: 81-107 <RES>
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                                                                                                                                                                                                                                                                                                                                                                           Keywords: phosphoprotein; RNA binding
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                                                                                                                                                         Local
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                                                                                                                            l Similarity
                                                              AALEAKICHQIEYYFGDF 18
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                            ribonucleoprotein repeat homology <RRM;
RNA-binding RNP2 motif
RNA-binding RNP1 motif
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                                                                                                                                                   100.0%; Score 99;
100.0%; Pred. No.
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RESULT 3

ribonucleoprotein La.A - African clawed frog N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Xenopus laevis (African clawed frog) C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change C;Accession: S33818; S28545

22-Jun-1999

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RESULT 5
S33818
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A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection A;Reference number: JC1494, MUID:93246255; PMID:7918708
A;Accession: JC1494
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                                                                                                                                                                                                                                                                                   F;111-177/Domain: ribonucleoprotein repeat homology <RRM:
F;112-117/Region: RNA-binding RNP2 motif
F;150-157/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                            ay act as a transcription termination factor.

C;Superfamily: ribonucleoprotein La. ribonucleoprotein []
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A; Residues: 1-427 <SCH>
A; Croos-references: EMBL: X68818; NID: g64875; PIDN: CAA48716.1; I
C; Comment: This protein associates with a variety of small RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: La proteins from Xenopus laevis. cDNA cloning and A; Reference number: $33817; MUID:93287095; PMID:8510143 A; Accession: $33817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S33817; S28544
R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson,
J. Mol. Biol. 231, 196-204, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change
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F;113-118/Region: RNA-binding RNP2 motif
F;151-158/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: liver C; Comment: This protein associates with a variety of small RNA molecules,
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A;Residues: 1-415 <SEM>
A;Cross-references: GB:X67859; NID:g55778; PIDN:CAA48043.1; PID:g55779
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C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                 C; Keywords: phosphoprotein; RNA binding
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A molecules,
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                                                                                                                                                                                                                                                                                                                                Database
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 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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x; cnan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A; Title: Ribonucleoprotein SS-B/La belongs to a protein A; Reference number: S03848; MUID:89202037; PMID:2468131
A; Accession: S03849
A; Molecula Free

family with consensus sequences

most

of which

22-Jun-1999

A; Molecule type: mRNA A; Residues: 1-404 < CHA> A; Cross-references: EMB

N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec:1990 #sequence_revision 26-May-1994 #text_change

ribonucleoprotein La - bovine

45	44	43	42	41	40	39	38	37	36	ဌ	34	33	32	31	30
41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	42
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helicase (EC 3.	റ			protein -	DNA-directed RNA			polymeras	catalase (EC 1.11.	RING	hypothetical prote		tolace-binding pro	н	۰,

ALIGNMENTS

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ribonucleoprotein La - human
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen
C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence revision 26-May-1994 #text change 22-Jun-1999
C;Accession: A31888; S03848; \( \bar{R}\)22956; A61051; S11013; I55\)553; I70205; I70206; A31273
R;Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A;Title: Genomic structure and amino acid sequence domains of the human La autoantigen.
A;Reference number: A31888; MUID:89053970; PMID:3192525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: This protein associates with a variety of small RNA molecules,
ay act as transcription termination factor.
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: blocked amino end; phosphoprotein; RNA binding
F;111-118/Domain: ribonucleoprotein repeat homology cRRM>
F;151-158/Region: RNA-binding RNP2 motif
F;151-158/Region: RNA-binding RNP1 motif
A;Molecule type: mRNA
A;Residues: 1-408 <CHA>
A;Residues: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687
A;Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687
R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with cons
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   Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
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100.0%; Pred. No.
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hypothetical Na+/H+ antiporter

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RESULT 15
Q91HL3
ID Q91HL
AC Q91HL
AC Q91HL
DT 01-QC
DT 01-QC
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QT 0
Search completed: September 10, 2004, 18:00:06 Job time: 44.229 secs
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Best Local S
Matches 9
                                                                                                                                                                                                                                            Query Match 46.4%; Score 45; DB 10; Length 455; Best Local Similarity 60.0%; Pred. No. 28; Matches 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP002041; BAB02607.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR00630; Lupus La dom.
InterPro; IPR005630; Lupus La dom.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF05383; La; 1.
PRINT; SM00076; rrm; 1.
PRINT; SM00076; rrm; 1.
SMART; SM000705; LUPUSIA.
SMART; SM000705; RRM; 1.
PROSSITE; PS50102; RRM; 1.
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STRAIN=Columbia;
Kaneko T., Kato T., S
Submitted (MAY-2000)
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Q91HL3;
Q14HC3;
Q15HC13;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA-binding protein-like.
RNA-binding protein-like.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                    455 AA;
                                                                                                                                                                                                                                                                                                                                                                    48958 MW; E88117B22C33BBA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato S., Nakamura Y., Asamizu E., Tabata ) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2002
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MEDLINE-01301, PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Surtton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococus furio submitted (FEB-2002) to the EMBL/GenBank/DDBJ EMBL; AE010164; AAL80539.1; -. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR002372; Bac_PQQ_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM;
SEQUENCE 343 AA; 376
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus furiosus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VUI9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00564; PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                     STRAIN=Berkeley;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                           CG10006
                                                                                                                                                                                                                                                                                                                                                                                                          CG10006 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALEAKICHQIEYQFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADIAQKIIKQVEYQFSD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALEAKICHQIEYQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWEGKICENIEYO 31
                                                                                                                                                                                                                                                                                                                                                                   melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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; 37628 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.48;
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13,
24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermococci;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB pred. No. 16; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            946EC9C97EE327D4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395
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                                                                                                                                                                                                                                                                                                                                             Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                       Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 343;
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COCCERTOR REPORTED BY SELECTION OF SELECTION
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolihakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadisu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Celbart W.M., Glasser K.,
RA Glodek A., Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Melson D.R., Nelson K.A., Nixon K., McDerson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Sunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Smith T.,
RA Yelson D.R., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelson S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelson D.R., Ra Kims G., Zheng L.,
RA Yelson S., Pan S., Zhou X., Zhou S., Zhou Q., Zheng L.,
RA Yelson S., Ra, Wyers B.W., Rubin G.M., Venter J.C.;
RTHE STORMS S., San S., San S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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acid-binding protein family.";
Sex. Plant Reprod. 13:127-134(2000)
EMBL; AF094825; AAF600075.2; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                       STRAIN=cv. topas; TISSUE=Late
Smykal P., Janotov I., Pechan
                                                                                                                                                                                                                                                                                                                         Brassica napus (Rape).
Eukaryota; Viridiplantae; Stra
Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016020; C:membrane; IEA.
GO; GO:0046873; F:metal ion transporter
GO; GO:0030001; P:metal ion transport; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9SEU9;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003532; AAF49687.1; -. FlyBase; FBgn0036461; CG10006.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9SEU9
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                                                                                                                                                                                                                                                                                              NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RBP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-binding
                                                                                                                                                  "A novel Brassica napus L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                           TISSUE=Late-uninucleate microspores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homolog
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                                                                                                                                                                                                                                                                                                                               Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                       Streptophyta; Embryophyta;
rta; eudicotyledons; core eu
                                                                                                                                                  pollen-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46;
Pred. No.
                                                                                                                                                                                   P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                             eudicots;
                                                                                                                                                                                                                                                                                                                                                                                        Tracheophyta;
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                                                                                                                                                           nucleic-
                                                                                                                                                                                                                                                                                                                                                                   rosids;
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RESULT 10
Q8XW47
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Best Local
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Best Local (
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
 Q8XW47;
Q8XW47;
01-MAR-2002
01-MAR-2002
01-JUN-2003
Probable 2-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q95KA5; PRELIMINARY;
Q95KA5; PRELIMINARY;
01-DEC-2001 (TrEMBLrel. 19,
01-DCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                              libraries.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ database EMBL; AB063029; BAB60771.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0046873; F:metal ion transporter activity; IEA.
GO; GO:0030001; P:metal ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "NEDO human cDNA sequencing project.";
submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO55061; BAB70948.1; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0046873; F:metal ion transporter activity; IEA.
GO; GO:0030001; F:metal ion transport; IEA.
InterPro; IPR003689; Zn_transpt_Zip.
Ffam; PF02535; Zip; 1.
Pram; PF02535; Zip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nis Kimura K., Yamashita H., Matsuo K., Makamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K. Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suguano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
                                                                                                                                                                                                                    Hypothetical
SEQUENCE 6
                                                                                                                                                                                                                                         Pfam; PF02535; Zip; 1.
                                                                                                                                                                                                                                                    InterPro; IPR003689; Zn_transpt_Zip
                                                                                                                                                                                                                                                                                                                                         TISSUE=Medulla oblongata;
TSSUE=Medulla oblongata;
Tssuzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 65
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                                                                                                                                                                    7; Conserv
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002 (TrEMBLrel. 20, Last sequence update)
003 (TrEMBLrel. 24, Last annotation update)
2-amino-4-hydroxy-6-hydroxymethyldihydropteridine
                                                                                                                        AILCHEIPHEMGDF 552
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                                                                                                                                                                                                                    al protein.
654 AA; 7
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654 AA; 7
           (TrEMBLrel.
(TrEMBLrel.
                                                            PRELIMINARY;
                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                      72793 MW;
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50.0%;
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Last annotation updat
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Pred. No. 19;
4; Mismatches
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Pred. No.
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01-DEC-2001
01-DEC-2001
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GO; GO:0003848; F:2-amino-4-hydroxy-6-hydroxymethyldihydropte...
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0019396; P:folic acid and derivative biosynthesis; IEA.
InterPro; IPR000550; Hppk.
Pfam; PF01288; HPPK; 1.
TIGRFAM45; TIGR01498; folk; 1.
PROSITE; PS00794; HPPK; 1.
Transferase; Complete proteome.
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"Genome sequence of the plant pathogen Ralstonia solanacearum Nature 415:497-502 (2002).
                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Ga
Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin
Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S
White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
                                                  Pfam; PF05383; La; 1.
                                                                                                                                                                                                                                                 SUDMITTED (MAY-2001) to the EMBL; AC084404; AAK50577.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative RNA-binding protein.
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FOLK OR RSC2628 OR RS00932.
                                          Pfam; PF00076; rrm;
                                                                                        InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom
interPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                         GO; GO:0005634; C:nucleus; IEA
GO; GO:0003723; F:RNA binding;
                                                                                                                                                                                                                            Gramene;
                                                                                                                                                                                                                                                                            "Oryza sativa chromosome 3 BAC OSJNBa0026A15 genomic sequence."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice)
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Burkholderiaceae; Ralstoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ralstonia solanacearum (Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pyrophosphokinase ,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase
pxotein (BC 2.7.6.3).
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                        LUPUSLA
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18179 MW;
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Pred. No. 6.
                                                                                                                              dom
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6.8;
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Q7ZTIO;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TYEMBLYE1. 06, Created)
01-OCT-2003 (TYEMBLYE1. 25, Last sequence update)
01-OCT-2003 (TYEMBLYE1. 25, Last annotation update)
Hypothetical protein C14C6.12.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to sjogren syndrome antigen B (Autoantigen La).
Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
SEQUENCE 401 AA; 46138 MW;
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GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                  David M., Wohldmann P., "The sequence of C. elec
Submitted (JAN-1998) to
                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
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                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                               STRAIN-Bristol N2;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Wilson R.;
                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
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InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                    P., Bauer C., Antoniou B.; elegans cosmid C14C6."; to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.71;
1; Mismatches 4
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Q96NN4;
01-DEC-2001
01-DEC-2001
01-JUN-2003
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Q7XT99;
01-OCT-2003
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

FU G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,

Fu G., Wang S.Y., Ren S.X., Lv G., Chen J., Kang H., Chen X.Y.,

Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,

Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,

Shao Y., Sun J., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,

Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,

Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,

Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,

Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,

Zhang R.Q., Guan J.P., Hong G.F.;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                   Hypothetical
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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               TISSUE=Brain;
                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                        SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=9606;
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NCE 1560 AA; 177753 MW;
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7; Conserv
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Nakagawa
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(TrEMBLiel. 24, Last annotation update)
( protein FLJ30499.
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                                                                                                                                 Chordata;
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; 1.
SEQUENCE 415 AA; 47657 MW; A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AKO86677; BAC40499.1; ...
MGD; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La.
InterPro; IPR005630; Lupus_La.
InterPro; IPR005630; Lupus_La.
Ffam; PF05183; La; 1.
Pfam; PF05183; La; 1.
  Q7ZTK2;
Q7ZTK2;
01-JUN-2003
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01-QCT-2003
Similar to 1
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Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
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STRAIN-NOD; TISSUE-Thymus;

MEDLINE-2234683; PubMed=12466851;

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the most changeriptome based on functional annot 60,770 full-length cDNAs";

Nature 420:563-573(2002).
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
5jogren syndrome antigen B.
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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01-MAR-2003
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InterPro; IPR006630; Lupus La_dom
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                  ALEAKICHQIEYYFGDF 28
                                                                                                                                                                                                                                                                           ALEAKICHQIEYQFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALEAKICHQIEYYFGDF
(TrEMBLrel. 24, 0
(TrEMBLrel. 24, 3
(TrEMBLrel. 25, 3
lupus LA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 AA; 43891 MW;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.7%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
Last sequence update)
Last annotation update)
homolog B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                       Created)
                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                Score 87;
Pred. No.
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   A7545C7686AC8363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2E2DEF1452C0F0E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                    427
                                                                                                                                                                                                                                                                                                                                             DB 11;
1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
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LESKICQQIEYYFGN

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RESULT 4

RESULT 4

RESULT 4

RESULT 4

RESULT 01-0

RESULT 01-1-1

RESULT 01-0

RESULT 01-0

RESULT 02-0

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                                                                                Query Match
Best Local S
Matches 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

L'Ecuyer T.J., Fang H.-L.;

EMBL, AF467897; AAL/76269.1; -.

GO; GO:00035634; C:nucleus; IEA.

GO; GO:0003763; F:RNA binding; IEA.

InterPro; IPR006304; Lupus La_dom.

InterPro; IPR006504; RNA_rec_mot.

Pfam; PF00383; La; 1.

Pfam; PF00383; La; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
SMO0360; RRM; 1.
SPROSITE; PS50102; RRM; 1.
SEQUENCE 427 AA; 48996 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8QHI5 PRELIMINARY; PRT; 206 AA.
Q8QHI5;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Untranslated region binding-protein.
                                                                                                                                                                                                                                       PROSITE; PS00102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; 1.
SROUTENCE 206 AA; 23992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC046654; AAH46654.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La.
InterPro; IPR005630; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S., Strausberg R.;
Submitted (FEB-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
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                                                                                                                          Similarity
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LEAKICHQIEYQFGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDTKICEQIEYYFGD
                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Weognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                     62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.9%;
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                                                                       Score 61; DB 13; Pred. No. 0.022; Mismatches
                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases.
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Pred. No. 0.03
1; Mismatches
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                                                                                                                                                                                                                                                    965B62F7DFFB90E9 CRC64;
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0.032;
                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                Length 206;
                                                                                        Indels
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Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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        September 10, 2004, 17:29:01; Search time 41.229 Seconds (without alignments)
137.751 Million cell updates/sec
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97
                                                                                                                                                                                        SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
sp_mammal:*
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sp_phage:*
sp_plant:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_vertebrate:*
sp_bacteriap:*
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                                                                                                                                                              sp_human:*
sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	6	_U	4.	w	N	1	Result No.
45	4 5	45	46	46	46	46	47	47	48	49	54	61	62	87	87	Score
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10	10	10	ហ	17	10	16	Ø	4	10	v	13	13	13	11	11	!
Q9FRN9	Q9LHL3	Q9SEU9	Q9VUI9	Q8U3P2	Q94LD0	Q8XW47	Q95KA5	Q96NN4	Q7XT99	044678	Q7ZTI0	Q8QHI5	Q7ZTK2	Q8BTU4	Д9С ҮВ9	ID
Q9frn9 oryza sativ	Q9lhl3 arabidopsis	Q9seu9 brassica na	Q9vui9 drosophila	Q8u3p2 pyrococcus	Q941d0 oryza sativ	Q8xw47 ralstonia s	Q95ka5 macaca fasc	Q96nn4 homo sapien	Q7xt99 oryza sativ	044678 caenorhabdi	Q7zti0 brachydanio	Q8qhi5 gallus gall		Q8btu4 mus musculu	Q9cyb9 mus musculu	Description

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45.4	45.4	45.4		45.4	45.4	45.4	•	45.4	•	45.4	•	٠	٠	45.4	45.4	45.4	45.4	45.4	45.4	45.4		45.4	45.4	45.4	45.4	տ	45.4	
1381	1230	835	765	765	749	701	661	660	647	626	582	571	568	567	539	535	535	505	433	382	381	230	228	160	149	129	96	1456
10	10	4	11	11	4	v	11	11		4		σ				11			4	4	11			4.			10	
Q84JZ9	Q9LD66	Q9ULF5	Q7TPP9	Q8C145	Q13433	Q9VSL7	Q80TG2	Q9DAT9	Q9H6T8	Q9NXC4	Q7TQE0	Q7Z1R8	Q9KKL7	Q7X6F9	Q8N6Y3	Q9D909	Q9D856	Q8R518	Q8IXR3	Q96HP5	Q8BX42	Q8CHL4	Q8C0L2	Q8NC35	Q9NX22	Q96MI3	Q9AUG1	Q7X975
Q84jz9 oryza sativ	oryza sat	nomo sa	Q7tpp9 mus musculu	mus	homo	dros	Q80tg2 mus musculu	mus	homo	homo	enm 0	=	~1	oryz	Q8n6y3 homo sapien	mus	mus	Bru	nomo	Domo	2 mus	mus	mus	Omo	homo	nomo	l bras	

ALIGNMENTS

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Matches
                                                    Query Match
Best Local
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Pfam; PF00122; E1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
Pfam; PF007019; CATATPASE
PRINTS; PR00119; CATATPASE
PRINTS; PR00120; HATPASE
TIGRPAMS; TIGR01524; ATPase-IIIB Mg; 1.
TIGRPAMS; TIGR01524; ATPASE E1 E2; 1.
PROSITE; PS00154; ATPASE E1 E2; 1.
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DOMAIN
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InterPro; IPR006415; ATPase-IIIB Mg.
InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR004014; Cation_ATPase_N.
InterPro; IPR008250; E1-E2_ATPase_reg.
InterPro; IPR00955; HATPase.
InterPro; IPR005834; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U07843; AAA68988.1; -. EMBL; AE008909; AAL23275.1; PIR; B57147; B57147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long a
modified and this statement is not removed.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
-!- FUNCTION: Mediates mag-
-!- CATALYTIC ACTIVITY: A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Magnesium; Transmembrane; Phosphorylation; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +
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SUBCELULIAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the cation transport ATPA
ATPases). Subfamily IIIB.
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6; Conserv
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10 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

MAGNESIUM (POTENTIAL).

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7 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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5 (POTENTIA)
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37;
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Best Local S
Matches 6
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15-DEC-1998
15-DEC-1998
10-OCT-2003
                                                                                  is-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trans-cinnamate 4-monoxygenase (EC 1.14.13.11) (Cinnamic acid
4-hydroxylase) (CA4H) (P450C4H) (Cytochrome P450 73).
Cyp73A10 OR CYP73.
Petroselinum crispum (Parsley) (Petroselinum hortense).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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campanulids; Apiales; Apiaceae; Apioideae; apioid Apium clade; Petroselinum.
NCBI_TaxID=4043;
[1]
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PROSITE; PS50822; PIWI; 1.
Developmental protein; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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TISSUE SPECIFICITY: Widely expressed at low levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR
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AC007932; AAD49755.1; -.
AC020889; AAF79718.1; AI
BT000941; AAN41341.1; -.
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K., Davis R.W., Theologis A.,
s of transcriptional activity i
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MW; 3E5146343A09C541 CRC64;
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Pred. No. 29;
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P36640;
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O1-JUN-1994 (Rel. 2
10-OCT-2003 (Rel. 4
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Logemann E., Parniske M., Hahlbrock K.;
Logemann E. Parniske M., Hahlbrock K.;
Modes of expression and common structural features of the complete
"Modes of expression and common structural features of the complete
phenylalanine ammonia-lyase gene family in parsley.";
Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909 (1995).
-!- FUNCTION: Controls carbon flux to pigments essential for
pollination or UV protection, to numerous pytoalexins synthesized
by plants when challenged by pathogens, and to lignins.
-!- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-.
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., LeCOURTHLY L., Porwollik S., Ali J., Dante M., Du F., Hou S. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan Waterston R., Wilson R.K.;
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                                                                                                                            STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                      Tao T., Snavely M.D., Fa "Magnesium transport in ATPase and is regulated mgtB P-type ATPase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95270580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGTA OR STM4456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mg(2+) transport ATPase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                          2
                                                                                                                                                                                                                                 Bacteriol. 177:2654-2662(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro; IPR001128; Cytochrome_P450
PF00067; P450; 1.
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6; Conserv
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42, Last annotation updat
ATPase, P-type 1 (EC 3.6.2
                                                                                                                                                                                                                                                                                                                                                         PubMed=7751273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29, Created)
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                                                                                                                                                                                                                                                                           Farr S.G., Maguire M.E.;
in Salmonella typhimurium: mgtA encodes
ed by Mg2+ in a manner similar to that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
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Pred. No.
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3.6.3.2)
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S., Layman
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                                                                                                                                                                                                                                                                                        of the
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                                                                                   ceille P.,
Layman D.,
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L outstation -
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SGD; S0003320; CTT1.

GO; GO:0006950; P:response to stress; III
InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOm; PD000510; Catalase; 1.
PROSITE; PS000437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
Oxidoreductase; Peroxidase; Iron; Heme;
                                                                                                                                                                                                                                                                    EMBL; X04625; CAA28298.1; -.
EMBL; Z72873; CAA97090.1; -.
EMBL; Z72873; CAA974540.1; -.
PIR; S64383; CSBYI.
HSSP; P040400; IF4J.
CSBYT.
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Multigene family.
ACT_SITE 75
ACT_SITE 148
                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norbeck J., Blomberg A.; "Metabolic and regulatory changes associated with growth of "Metabolic and regulatory changes associated with growth of Saccharomyces cerevisiae in 1.4 M NaCl. Evidence for osmotic induction of glycerol dissimilation via the dihydroxyacetone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 405-409.
STRAIN=ATCC 44827 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86230135; PubMed=2423850; Spevak W., Hartig A., Meindl P., Ruis "Heme control region of the catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-74 FROM N.A. MEDLINE=86230135; PubMed=2
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Hernandez K., Weber N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of the Saccharomyces cerevisiae deduced amino-acid sequence of yeast catalase T."; Eur. J. Biochem. 160:487-490(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 12-573
MEDLINE=87053966; E
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                     GermOnline; 141400; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic.
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Occurs in almost all aerobically respiring organisms
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PubMed=3536508;
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the EMBL/GenBank/DDBJ
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A8
    SIMILARITY.
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RX Theologis A., Ecker J.R., Palm C.J., Pederspiel N.A., Kaul S.,
RA Theologis A., Ecker J.R., Palm C.J., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Dubler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Lid J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Nil H., Salzberg J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
When J., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Georgies and Analysis of Arromosome 1 of the New Alant Arabidonsis
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004379; Q9LP83;
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16-OCT-2001 (Rel
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SEQUENCE
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F., Karlin Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G., Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J., Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Arakawa T., Banh J., Banno F., Bowser L., Gurjal M., Hansen N.F., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F., Hayashizaki Y., Johnson-Hopson C., Hauan V.W., Ida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
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AGO1 OR AT1G48410 OR F11A17.3 OR T1N15.2.
                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
MEDLINE=22954850; PubMed=14593172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bohmert K., Camus I.,
"AGO1 defines a novel
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090460; PubMed=9427751;
, Camus I., Bellini C., Bouchez D., Caboche M., Benning
nes a novel locus of Arabidopsis controlling leaf
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Pred. No. 16;
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E03380543767377B CRC64;
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                                                                                                                                                                                       Toriumi M.J.,
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RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.N.
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
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                                                                                                                                                                                                                                                                                                                            EMBL; U39703; AAC71469.1; -.

BR EMBL; X61535; CAB88133.1; -.

BR PIR; E64227; E64227.

BR HSSP; P00579; E64227.

BR HSSP; P00579; 1SIG.

BR TIGR; MG249; -.

BR TIGR; MG249; -.

BR InterPro; IPR007627; Sigma70_r2.

BR InterPro; IPR007624; Sigma70_r3.

BR InterPro; IPR007624; Sigma70_r3.

BR InterPro; IPR000943; Sigma70_r3.

BR FAGSITS; P604542; Sigma70_r3; 1.

BR PAGSITS; P800716; SIGMA70_T3; 1.

BR PROSITS; P800716; SIGMA70_Z; 1.

BR PROSITS; P800716; SIGMA70_Z; 1.

BR PROSITS; P800716; SIGMA70_Z; 1.

BR PROSITS; PS00716; SIGMA70_Z; 1.

BR PROSITS; PS00716; SIGMA70_Z; 1.

BR PROSITS; PS00716; SIGMA70_Z; 1.
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA polymerase sigma factor rpoD (Sigma-A).
RPOD OR SIGA OR MG249.
                                                                                                                                                                                                      DNA_BIND
CONFLICT
SEQUENCE
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STRAILAFATCC 33530 / G-37;
MEDILINE=92051396; PubMed=1945886;
Peterson S.N., Schramm N., Hu P.-C., Bott
"A random sequencing approach for placing
of Mycoplasma genitalium.";
Nucleic Acids Res. 19:6027-6031(1991).
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01-FEB-1996 (Re
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). \hfill \hfi
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                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                              DNA-binding;
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                                                 ALEAKICHQIEYQFGDF
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Pred. No.
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H-T-H MOTIF (BY SIMILARITY).
DPESEQRIA -> NLNSGLP (IN REF. 2).
ADE06CA668F59A65 CRC64;
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physical map
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CATT_YEAST ST
ID CATT_YEAST ST
AC PO6115;
DT 01-JAN-1988 (Rel.
DT 01-OCT-1996 (Rel.
DT 28-FEB-2003 (Rel.
DE Catalase T (EC 1.
GN CTT1 OR YGR088W.
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RPSD_MYCPM
ID RPSD M
AC P78072
DT 01-NOV
DT 01-NOV
DT 01-NOV
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OC Bacter
OX NCB1 I I
RR NI II
RR HITMMel
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MEDLINE-97105885; PubMed=8948633;
MEDLINE-97105885; Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR009043; RNA_pol_sigma.
InterPro; IPR007627; Sigma70_r2.
InterPro; IPR007624; Sigma70_r3.
InterPro; IPR007624; Sigma70_r3.
InterPro; IPR00943; Sigma70_r3.
InterPro; IPR00942; Sigma70_r2; 1.
Pfam; PF04539; Sigma70_r3; 1.
PRINTS; PR00046; SIGMA70PCT.
PROSITE; PR00715; SIGMA70PCT.
PROSITE; PS00716; SIGMA70_2; 1.
PROSITE; PS00716; SIGMA70_2; 1.
PROSITE; PS00716; SIGMA70_2; 1.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA polymerase sigma factor rpoD (Sigma-A).
RPOD OR SIGA OR MPN352 OR MP484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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HSSP; P00579; 1SIG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000047; AAB96132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the sigma-70 factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: The sigma factor is an initiation factor that attachment of the RNA polymerase to specific initiation then is released. This is the primary sigma-factor of the bacteria (By similarity).
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                 ALEAKICHQIEYQFGDF 18
                             (Rel. 06, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat
(EC 1.11.1.6).
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453
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276 289 PC
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3; Mismatches
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H-T-H MOTIF (BY SIMILARITY)
; 7981C3EBDEF7C1E1 CRC64;
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McCherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Mcris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Melson K.A., Nixon K., Musskern D.F., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paccleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Stence 287:2185-2195(200).
                                                              Query Match
Best Local S
Matches 8
                                                                                                                                                                                                               PRINTS; PRO0302; LÚPUSLA.

SMART; SM00715; LA; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM RNP 1; 1.

RNA-binding; Nuclear protein; D

DOMAIN 149 234 RN
                                                                                                                                 CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0011638; La.
GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.
GO; GO:0003723; F:RNA binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L32988; AAA21776.1; -.
EMBL; AE003666; AAF53885.1; -.
EMF; A53773, A53773.
PIR; A53781; A53781.
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EMBL; L32988; AAA21776.1; -.
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SIMILARITY: Contains 1 RNA recognition motif (RRM)
SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (Probable).

DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo followed by a restricted pattern of mesodermal expression that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May be involved in transcription termination polymerase III. Binds RNA and DNA. Binds to precursors polymerase III transcripts. May play a specialized role
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                                                              Similarity
8; Conserv
ERAIIRQVEYYFGD
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182
283
329
390 /
                                                              Conservative
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183
283
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                                                                              44.3%;
64
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                                                                              Score 43;
Pred. No.
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A -> T (IN REF
                                                                                                                                                X - >
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N (IN REF. 1).
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                                                                                              Length 390;
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01-AUG-1990
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MEDLINE=90385281; PubMed=2402637;
Schumann R.R., Leong S.R., Flaggs G.W., Gray P.W., Wright S.D.,
Mathison J.C., Tobias P.S., Ulevitch R.J.;
"Structure and function of lipopolysaccharide binding protein.";
                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00400; LBP BPI CETP; 1.
Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 26
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO01124; LBP_BPI_CETP pfam; PF01273; LBP_BPI_CETP; 1. Pfam; PF02886; LBP_BPI_CETP_C; 1. SMART; SM00328; BPI1; 1. SMART; SM00329; BPI2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35534; AAA99235.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 249:1429-1431(1990).
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Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P17213; 1BP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B35843; B35843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of a lipopolysaccharide-binding acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tobias P.S., Soldau K., Ulevitch R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=86306528; PubMed=2427635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipopolysaccharide-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Binds to the lipid a moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. The LBP/LPS complex so to interact with the CD14 receptor.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.
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                                                                                       Similarity
8; Conserv
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                                                                                                          43.3%;
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PI_CETP; 1.
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                                                                                                        Score 42;
Pred. No.
                                                                                                                                                                                                    LIPOPOLYSACCHARIDE-BINDING PROTEIN.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

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E -> G (IN REF. 2).

S -> F (IN REF. 2).
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                                                                                         Mismatches
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precursor (LBP)
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PROSITE; PS50102; RRM RNP 1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
RNA-binding; Nuclear protein; Phosphorylation.
DOMAIN 111 203 RNA-BINDING (RRM)
DOMAIN 196 212 NUCLEAR LOCALIZAT
DOMAIN 316 332 NUCLEAR LOCALIZAT
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                  use by non-profit institu modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                        Pardigon N., Strauss J.H.;
"Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";
J. Virol. 70:1173-1181(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                InterPro; IPR000504; Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                            This SWISS-PROT between the Swi
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=96135233; PubMed=8551578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          La protein homolog (La ribonucleoprote
Aedes albopictus (Forest day mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05383; La; 1.
                                                          InterPro; IPR002344; InterPro; IPR006630;
                                                                                        EMBL; S80954; AAB35931.1;
                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEDAL
                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                       amounts are present in the cytoplasm. SIMILARITY: Contains 1 RNA recognition motif SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                               FUNCTION: May be involved in transcription termination by FUNCTION: May be involved in transcription termination by Functions are single for the 3' end of the involved for the strand of Sindbis virus RNA. This may be significant Sindbis virus RNA replication.
                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Nuclear. Primarily nuclear,,
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                PF05383; La; 1. PF00076; rrm; 1
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   PR00302; LUPUSLA
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428
                                                                                                                     equires a license agreement email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
nomolog (La ribonucleoprotein) (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                          ; Lupus_La.
; Lupus_La_dom.
; RNA_rec_mot.
                                                                                                                                                  institutions as long as its content atement is not removed. Usage by an
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0.019;
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RESULT 8
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Best Local S
Mainhes 9
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gerge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gerger Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Choston K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorbon K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE
RNA-binding; Nuclear protein; DNA-E
DOMAIN 141 228 RNA-BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Canton-S; TISSUE=Ovary;
MEDLINE=94309632; PubMed=8035794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologous to the human systemic lupus La/SS-B autoantigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bai C., Li Z., Tolias P.P.;
"Developmental characterization of a Drosophila RNA-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
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ll. Biol. 14:5
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383 AA; 44430 MW; 4E5CC8F21C40F452
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1; Mismatches
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Matches 16
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01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Lupus La protein homolog B (La ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAB_XENLA
P28049;
              This
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PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Nuclear protein; P
DOMAIN 111 187 RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
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                                                                                                                                         \frac{1}{1} \frac{1}{1}
                                                                                                                                                                                                                                        expression.";
                                                                                                                                                                                                                                                     MEDLINE=93287095; PubMed=8510143;
Scherly D., Stutz F., Lin-Marq N., Clarkson S.G.;
"La proteins from Xenopus laevis. cDNA cloning and developmental
                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve;
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                LAB1.
                                                                                                                                                                                                                                                                                                                                                                                                                              homolog B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:98423; S8b.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR009504; RNA_rec_mot.
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EMBL; BC003820; AAH03820.1;
EMBL; Y07951; CAA69249.1; -.
                                                                                                                                                                                                                                                                                                   TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355,
                                                                                                                                                                                                                                                                                                                                                          Xenopodinae;
                                                                                                        401. Biol. 231:196-204(1993).

*FUNCTION: La protein plays a role in the transcription of RNA PUNCTION: La protein plays a role in the transcription termination polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).

SUBCELLULAR LOCATION: Nuclear (Probable).

DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly accumulate in stage III/IV nascent plays and early
                                    PTM: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of La, LaA and LaB, in :
SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALEAKICHQIEYQFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                       Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH03820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47756 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
ia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 415;
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through a c
d the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                        (La
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    a collaboration
MBL outstation -
                                                                     in xenopus
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RESULT 6
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Best Local S
Matches 11
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.

PROSITE; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAA XENLA
P28048;
                                                              This
                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                         MEDLINE-93287095; PubMed=8510143;
Scherly D., Stutz F., Lin-Marq N.,
"La proteins from Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Cranita; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-MAR-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There by non-profit institutions as not removed. I modified and this statement is not removed. I entities requires a license agreement (See httentities requires a license agreement)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68818; CAA48716.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homolog A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lupus La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002344;
InterPro; IPR006630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR000504;
                                                                                                                                                                                                            polymerase III transcripts (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly constant steady state level in mature oocytes, eggs, and earl
                                                                                                                      PTM: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of La,
SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN
                                                                                                       SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                    European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S33817;
                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation surropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
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004 (Rel. 43, Last annotation updat
protein homolog A (La ribonucleopr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAKICHQIEYQFGD
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Bioinformatics Institute. The profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S33817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23,
43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Lupus_La.
; Lupus_La_dom.
; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation update)
(La ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62; DB 1;
Pred. No. 0.0039
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA-BINDING (RRM).
NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45F3146F8934A355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clarkson S.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                in the transcription of RNA
                                                                                                                                                                                                                                                                                                                        a transcription termination virtually all nascent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; I
ia; Pipoidea;
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ng as its content is in
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no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi; 
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (La
                                                                                                                                                    LaB,
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00030; RRM_RNP_1; 1.
Systemic lupus erythematosus; RNI
Nuclear protein.
DOMAIN 111 187 RNA
MOD RES 366 366 PHO:
SEQUENCE 408 AA; 46837 NW; EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995
01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                              or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation of rat cDNA clones coding for the detection of species-specific variations."; Gene 126:265-268(1993)
                        PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation
DOMAIN 111 187 RNA-BINDING (RRM;
                                                                                                                  SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93246255; PubMed=7916708; Semsei I., Troester H., Bartsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSB OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, La:
28-FEB-2003 (Rel. 41, La:
2005 La protein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P38656;
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  SEQUENCE
                                                                                                                                                                 PRINTS; PR00302; LUPUSLA.
                                                                                                                                                                                       Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                     InterPro; IPR000504;
                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                            PIR; JC1494;
                                                                                                                                                                                                                                                                                                                                EMBL; X67859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bachmann M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Interacts with DDX15 (By similarity) SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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                                                                                                                                                                                                                                                                                                                                                                              requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                              IPR006630;
                                                                                                                                                                                                                                                                                 IPR002344;
  415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                            JC1494.
                                                                                                                                                                                                                                                                                                                                  CAA48043.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31, Last sequence update)
41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
  47777 MW;
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                                                                                                                                                                                                                                   Lupus_La_dom.
RNA_rec_mot.
                                                                                                                                                                                                                                                                                    Lupus_La.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-BINDING (RRM).
PHOSPHORYLATION (BY CK2).
; EC153C15F9187FC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribonucleoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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  033FD9CC1E475F98
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3.5e-08;
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RESULT 4
LA_MOUSE
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X La, Hong L., Soures M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Rillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Yallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Althing M., Madan A., Young A.C., Shevch
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Best Local
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01-OCT-1993
15-MAR-2004
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P32067;
                                     This
                                                                                                                          -!- SUBUNIT: Interacts with DDX15 (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- PITM: Phosphorylated (By similarity).
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Groelz D., Bachmann M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reactivity of recombinant protein autoantibodies.";
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Topfer F., Gordon T., McCluskey J.;
"Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding site and conserved RNA-binding site an
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MEDLINE=93203630; PubMed=8454877;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                             mitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor form
of RNA polymerase III transcripts including tRNA and 4.55, 55, 7
    SWISS-PROT entry is copyright.
een the Swiss Institute of Bio
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(Rel.
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257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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27,
43,
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Last annotation update)
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    Bioinformatics
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                                                                                                                                                                                                             RX MEDLINE=22388257, PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Celbins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Wassen M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.;
Interpolation and initial analysis of more than 15,000 full-length
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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14- Lupus La protein (Sjogren syndrome to

14- Lupus La protein) (La autoantigen)
                                                                                              Sturgess A.D.,
Coppel R.S.;
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Chambers J.C., Kenan D., Martin B
"Genomic structure and amino acid
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Mammalia; 1
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                                                                                                                                                MEDLINE=88199081;
                                                                                                                                                                             SEQUENCE OF
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    Last sequence update)
    Last annotation update)

                                                                                                                                                      PubMed=2452201;
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ivan K.F., Tan E.M.;
                                                                                                                                                                             FROM
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Primates;
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                                                                                                                      McNeilage L.J.,
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Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S. Van Venrooij W.J., Pruijn G.J.M.;
"The human La (SS-B) autoantigen interacts with DDX15/hPrp43, putative DEAH-box RNA helicase.";
RNA 8:1428-1431(2002).
-!- FUNCTION: La protein plays a role in the transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
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                    SMART; SM00715; LA;
SMART; SM00360; RRM;
                                                                                      Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                           GO; GO:0030529; C:ribonucleoprotein complex; TASGO; GO:0003729; F:mRNA binding; TAS.GO; GO:0000049; F:tRNA binding; TAS.GO; GO:00008334; P:histone mRNA metabolism; TAS.GO; GO:0008334; P:tRNA modification; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04205; AAA51885.1; -.
EMBL; BC001289; AAH01289.1;
EMBL; BC020818; AAH20818.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                    PRINTS;
                                                                                                                                            InterPro;
                                                                                                                                                             InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
                                                                                                                                                                                                                                                                                                                                      MIM; 109090;
                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:11316; SSB.
                                                                                                                                                                                                                                                                                                                                                                                    PIR; A31888; A31888.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH DDX15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: The N-terminus is blocked.

DISEASE: Sera from patients with systemic lupus erythematosus often contain antibodies that react with the normal cellular La protein as if this antigen was foreign.

SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts including tRNA and 4.5S, 5S, of RNA polymerase III transcripts 
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear (Probable) PTM: PHOSPHORYLATED. THE PHOSPHORYLATION C-TERMINAL PART OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and 7-2 RNAs.
SUBUNIT: Inte
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RRM; 1.
                                                                    LUPUSLA
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129.452 Million cell updates/sec
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CARA BUCGN
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CARA BUCGN
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P66115 saccharomyc
O04379 arabidopsis
Q4303 petroselinu
P36640 salmonella
Q9xgw1 arabidopsis
P59576 buchnera ap
O14879 homo sapien
O84883 chlamydia t
P46735 mus musculu
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P05455 homo sapien
P38656 rattus norv
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                                                                                   1 homo sapien
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7 nicotiana t
4 rickettsia
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EMBL; X13698; CAA31986.1; -.

plr; S03849; S03849.

InterPro; IPR002344; Lupus_La_dom.

InterPro; IPR00630; Lupus_La_dom.

InterPro; IPR00504; RNA_rec_mot.

PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.

PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.

Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.

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BOSS taurus (Bovine). Bos taurus (Bovine). Bukaryota; Metazoa; Chordata; Craniati Mammalia, Eutheria; Cetartiodactyla; l Bovidae; Bovinae; Bos. NCBI TaxiD=9913; ISSUE=Pituitary; MRDINIB=89202037; PubMed=2468131; MRDINIBERD=802031; MRDINIBERD=802031; MRDINIBERD=80202031; MRDINIBERD=80202037; MRDINIBERD=80202037; MRDINIBERD=80202037; MRDINIBERD=80202037; MRDINIBERDERD=802020; MRDINIBERDERD=802020; MRDINIBERDERD=80202037; MRDINIBERDERD=802020; MRDINIBERDERD=80202020; MRDINIBERDERD=80202037; MRDINIBERDERD=80202037; MRDINIBERDERD=802020; MRDINIBERDERD=802020; MRDINIBERDERD=80202020; MR	1036 1036 298 479 487 505 505 505 505 505 505 505 505 505 50
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Euteleostomi; cora; Bovoidea; lly with consensus intiption of RNA ion termination hascent h precursor forms and 4.5S, 5S, 7S, and 4.5S, 5S, 7S, the EMBL outstation the EMBL outstation orestrictions on ith ontent is in no wa by and for commercia ww.isb-sib.ch/announce	4 homo sapie 8 rattus nor 8 ratius nor 8 ratizosacc 0 arabidopsi 6 chlamydoph 4 arabidopie 18 cicer arie 19 glycyrrhiz 17 pisum sati 5 phaseolus 5 zinnia ele
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transcription initiation factor sigma A - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: hypothetical protein H91_orf499
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 27.Feb-197 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: 873810
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: 873327; MUID:97105885; PMID:8948633
A;Accession: 873810
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-499 <-HIM>
A;Residues: 1-499 <-HIM>
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Generics:
                                                                                                                                                                                                                                                                                                                                                  A;Gene: sigA
A;Genetic code: SGC3
A;Genetic code: SGC3
C;Superfamily: transcription initiation factor sigma katF homology
C;Keywords: DNA binding; sigma factor; transcription initiation
F;254-487/Domain: transcription initiation factor sigma katF homology <KTF>
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Search completed: September 10, 2004, 18:02:30 Job time : 16.0782 secs
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Best Local Similarity 47.1%;
Matches 8; Conservative
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: RNA binding
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R;YOO, C.J.; Wolin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a
A;Reference number: A53781; MUID:94309661; PMID:8035818
                                                                                                                                                                                                                     hypothetical protein C30H6.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Sep-2000 C;Accession: T19585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1
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Bubmitted to the EMBL Data Library, October 1995

Submitted to the sequence of C. elegans cosmid
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C;Date: 19-Jan-1996 #sequence_revi
                                      A; Experimental source: clone C30H6
                                                                                                                                         A;Reference number: Z19148
A;Accession: T19585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1131 <BEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C25F6.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A53781
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                                                           A;Cross-references: EMBL:Z81044; PIDN:CAB02806.1; GSPDB:GN00022;
                                                                                                 A; Molecule type: DNA
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                                                                              A;Residues: 1-360 <WIL>
                                                                                                                                                                               ubmitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Caenorhabditis elegans
;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
;Accession: T15617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F
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Best Local
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                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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  CESP: C30H6.2
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7; Conserva
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8; Conservative
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Pred. No.
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Query Match
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C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: E64227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M35534; NID:g165467; PIDN:AAA99235.1; PID:g165468 R;Tobias, P.S.; Soldau, K.; Ulevitch, R.J. Exp. Med. 164, 777-73, 1986 J. Exp. Med. 164, 777-73, 1986 A;Title: Isolation of a lipopolysaccharide-binding acute phase reactant A;Reference number: A46553; MUID:86306528; PMID:2427635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, Science 249, 1429-1431, 1990
A;Title: Structure and function of lipopolysaccharide binding protein.
A;Reference number: A35843; MUID:90385281; PMID:2402637
A;Accession: B35843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 27-55,'XG',58-62,'F',64-65 <TOB>
C;Superfamily: lipopolysaccharide-binding protein
C;Keywords: acute phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipopolysaccharide-binding protein - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1999
C;Accession: B35843; A46553
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A;Introns: 43/2; 67/3; 111/3; 149/3; 231/3
C;Superfamily: Caenorhabditis elegans hypothetical
F;252-485/Domain: transcription
                       C;Superfamily: transcription initiation factor sigma katf homology C;Keywords: DNA binding; sigma factor; transcription initiation
                                                                  A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                     C;Accession: E64
R;Fraser, C.M.;
                                                                                                                                                                                                                                                                                                                                                                            C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000 C;Accession: E64227
                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription initiation factor sigma A N,Alternate names: RNA polymerase sigma-A
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A; Residues: 1-482 < SCH>
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Matches
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Best Local
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Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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    initiation
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Pred. No. 28;
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Pred. No.
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                                                                                                                                 NID: g3844835;
  factor sigma katF homology
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38;
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43.3%;

Score 42;

DB 2;

Length 497;

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A;Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874 C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor.

c;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: phosphoprotein; RNA binding
                                                                              R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera patho A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82379
                                                                                                                                                                                                                                                                                                                                RESULT 7
C82379
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J. Mol. Ricl '
                                                                                                                                                                                                                                     response regulator VCA1086 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Apr-2003 C;Accession: C82379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B. submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid C14C6
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-568 <HEI>
A;Cross-references: GB;
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A;Experimental source: strain Bristol N2; clone C14C6
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Best Local S
Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, Mol. Biol. 231, 196-204, 1993
Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; PIDN:AAF96979.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KICHQIEYQFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156/3
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71.4%;
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Pred. No.
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Pred. No.
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                                                                                                                                pathogen Vibrio cholerae
                                                                                                                                                                                                 Gwinn, M.L.; Dodson, H.; Dragoi, I.; Sell
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                                                                                                                                                                                                                          R.J.
    RESULT 10
A53781
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A; Experimental source: C; Genetics:
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Mol. Cell. Biol. 14, 5123-5129, 1994
A;Title: Developmental characterization of a Drosophila RNA-binding
A;Reference number: A53773; MUID:94309632; PMID:8035794
A;Accession: A53773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 21-Dec_1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
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                                                                                                                      A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: leucine zipper; RNA binding
                                                                                                                                                                                                                                                                                                                                                         La/SS-B homolog D-la - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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A; Accession: G02273
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A; Residues: 1-390 < BAI >
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1995
                                                                                                                                                                        A;Gene: FlyBase:La
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                                                             Conservative
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42.9%;
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Pred. No.
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Pred. No.
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A;Map position: 2

A;Map position: 2

A;Introns: 22/3; 57/2; 115/3; 185/2; 209/2; 223/3; 264/3; 380/2

C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C;Keywords: phosphoprotein; RNA binding

F;112-178/Domain: ribonucleoprotein repeat homology <RRM>

F;113-118/Region: RNA-binding RNP2 motif

F;151-158/Region: RNA-binding RNP1 motif

F;228-408/Domain: phosphorylated #status experimental <PHY>
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A; Molecule type: mRNA
A; Residues: 279-342 c. RE3>
A; Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
C; Comment: This protein associates with a variety of small RNA molecules
ay act as a transcription termination factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457 R;Kohsaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka, J. Clin. Invest. 85, 1566-1574, 1990 A;Title: Fine epitope mapping the human SS-B/La protein: Identification of A;Reference number: I55553; MUID:90237237; PMID:1692037 A;Accession: I55553
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation analysis of cDNA clones expressing human lupus La antigen. A;Reference number: A22956; MUID:85166283; PMID:3856888
A;Accession: A22956
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R;Sturgess, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel,
J. Immunol. 140, 3212-3218, 1988
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Immunol. Lett. 22, 65-72, 1989
A;Title: Demonstration of an amino terminal La epitope recognized by human anti-La
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A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 174-224 <RE2>
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A; Residues: 81-107 < RES>
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A; Residues: 'E',55-287,'V',289-408 <STU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references: GDB:125359; OMIM:109090
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                                                                                                                 Conservative
                                                                                                                                          93.8%;
28
                                                                                                                 <u>.</u>.
                                                                                                                                              Score 91;
Pred. No.
                                                                                                                 Mismatches
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                                                                                                                 1; Indels
                                                                                                                                                                       Length 408;
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RESULT 3

ribonucleoprotein La.A - African clawed frog
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change
C;Accession: S33818; S28545

22-Jun-1999

RESULT S33818

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N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: JC1494; S25145
R;Semsei, I.; Troester, H.; Bartsch, H.; Schwemmle, M.; Igloi, G.L.; Bachmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 126, 265-268, 1993
A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection A;Reference number: JC1494; MUID:93246255; PMID:7916708
                                                                                                                                                                                                                                                                      ay act as a transcription termination factor.
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat
C;Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribonucleoprotein La.B - African clawed frog
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-
C;Species: Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: phospn F;112-178/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
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                                        á
                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876 C;Comment: This protein associates with a variety of small RNA molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression. A;Reference number: S33817; MUID:93287095; PMID:8510143 A;Accession: S33817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change C;Accession: S33817; S28544 R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G. J. Mol. Biol. 231, 196-204, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: liver C; Comment: This protein associates with a variety of small RNA molecules,
                                                                                                                                                                                                    F;150-157/Region:
                                                                                                                                                                                                                              F;112-117/Region:
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-427 <SCH>
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Best Local
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  LDTKICEQIEYYFGD
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                                                                                                                                                                              phosphorylated
                                                                                                                                                                                                      RNA-binding RNP1 motif
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Pred. No.
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Pred. No. 0.015;
1; Mismatches
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2e-07;
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PIR 78:*
1: pir1:*
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97
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	տ	4.	ω	N	ם	Result No.
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probable olfactory	hypothetical prote	protei	transpor	Mg2+-transporting	conserved hypothet	trans-cinnamate 4-						cal		transcription init		lipopolysaccharide	hypothetical prote	hypothetical prote	ribonucleoprotein	La/SS-B homolog D-	LIV-1 protein - hu	response regulator	hypothetical prote	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	ribonucleoprotein	Description

ALIGNMENTS

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A31888 A31888 ribonucleoprotein La - human N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antiger C;Species: Homo sapiens (man) C;Date: 21-May-1990 #sequence revision 26-May-1994 #text change 22-Jun-1999 C;Accession: A31888; S03848; Ā22956; A61051; S11013; I55553; I70205; I70206; A31273 C;Anchers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D. J. Biol. Chem. 263, 18043-18051, 1988 A;Title: Genomic structure and amino acid sequence domains of the human La autoantigen. A;Reference number: A31888; MUID:89053970; PMID:3192525 A;Accession: A31888 A;Molecule type: mRNA A;Residues: 1-408 <cha> A;Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687 R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989 A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences</cha>	Query Match 93.8%; Score 91; DB 1; Length 404; Best Local Similarity 94.4%; Pred. No. 2e-07; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 AALEAKICHOIEVOFGDF 18	A;Molecule type: mRNA, A;Residues: 1-404 <cha> A;Residues: 1-404 <cha> A;Residues: 1-404 <cha> A;Residues: 1-404 <cha> A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Cross-references: EMBL:X13698; NID:g756 by protein sequencing C;Comment: This protein associates with a variety of small RNA molecules, most of which c;Comment: This protein description factor: ay ac: as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: blocked amino end; phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology <rrm> F;113-118/Region: RNA-binding RNP1 motif F;151-158/Region: RNA-binding RNP1 motif F;228-404/Domain: phosphorylated #status predicted <phy></phy></rrm></cha></cha></cha></cha>	RESULT 1 \$03849 ribonucleoprotein La - bovine ribonucleoprotein SS-B N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: \$03849 #sequence_revision E.M. R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989 A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences A;Accession: \$03848; MUID:89202037; PMID:2468131 A;Accession: \$03849

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Hall N. Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C., Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J., Cronin A., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Hauser H., Hornsby T., Holroyd S., Horrocks P., Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A., Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-VPI-5482 / ATCC 29148;
MEDLINE-22550858; PubMed-12663928;
XU J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
                                                                                                                                                                                      MEDLINE=22255708; PubMed=12
Hall N., Pain A., Berriman
                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. PFE0230W.
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01-OCT-2003
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TIGRPAM8; TIGR01180; aman2_put; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 756 AA; 86621 MW; 3DB7A9066E9B45D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 299:2074-2076(2003).
EMBL; AE016930; AAO76139.1;
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Bacteroidaceae; Bacteroides.
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01-JUN-2003 (TrEMBLrel. 24, Las
01-JUN-2003 (TrEMBLrel. 24, Las
Conserved hypothetical protein.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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V., Bowman S., C
ted (SEP-2002)
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38.9%;
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Apicomplexa;
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Pred. No. 26;
4; Mismatches
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Last annotation update)
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RESULT 15
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Best Local S
Matches 8
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Best Local S
Matches 7
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R EMBL; AL529351; CAD51412.1; -.

R GG; GG:0005489; F:electron transporter activity; IEA.

R GG; GG:0005451; F:sugar porter activity; IEA.

R GG; GG:000511; F:sugar porter activity; IEA.

R GG; GG:0009401; P:phosphoenolpyruvate-dependent sugar phospho...

R InterPro; IPR000345; CyrC heme BS.

R InterPro; IPR00714; HPT Serp S.

R InterPro; IPR007114; HPT Serp S.

R InterPro; IPR007114; HPT Serp S.

R PROSITE; PS00190; CYTOCHROME C; 4.

R PROSITE; PS00190; CYTOCHROME C; 4.

R PROSITE; PS00589; PTS HPR SER; 1.

R PROSITE; PS00028; ZINC FINGER C2H2 1; 2.
                                                                                                                             Complete SEQUENCE
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Q87T57;
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                                                                                                                                                      EMBL; AP005073; BAC58476.1; -. membrane; IEA. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0008415; F:acyttransferase activity; IEA. GO; GO:0009244; P:lipopolysaccharide core region InterPro; IPR004960; LipA acyttrans. PF03279; Lip_A_acytrans; 1.
                                                                                                                                                                                                                                                                                    STRAIN=RIMD 2210633 / Serotype 03:K6;

MEDLLINE=22508454; PLDMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Prof
Vibrionaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last Sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Putative lipid A biosynthesis (kdo)2-(lauroyl)-lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00028; ZIN
Hypothetical protein.
SEQUENCE 2349 AA;
                                                                                                                                                                                                                                                                            distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                         distinct from that of V. cholerae."; Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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8; Conserv
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329 AA;
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EEQDARTCNEAIEYFVGD
                            QQQEAKICHQ-IBYYFGD
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                                                              Conservative
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                                                                                                                               37996 MW;
                                                                            46.68;
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                                                             Score 47.5; D
Pred. No. 13;
7; Mismatches
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Pred. No. 79;
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                                                                                                                               CRC64;
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RESULT
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Best Local
                                        STRAIN=cv. Columbia;
Rounsley S.D., Kaul S.,
Brandon R.C., Sykes S.M
Somerville C.R., Venter
Submitted (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                           080567; Q9C5X1;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat Expressed protein (Virf-interacting protein FIP1)
protein) (At2943970/F8E33.10).
AT2G43970 OR F6E13.10/AT2G43970.
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                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 91 AA; 10
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MEDLINE=99069613; PubMed=9851916;
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STRAIN=Bristol N2;
                                                                                               SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID=3702;
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Science 282:2012-2018(1998).
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                    SEQUENCE
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           Columbia;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
protein C14C6.12.
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                     N.A.
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C. elegans control to the !
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cosmid C14C6.";
EMBL/GenBank/DDBJ
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Pred. No. 1.5;
1; Mismatches
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                                          EMBL/GenBank/DDBJ databases
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                                                              Ketchum K.A., Crosby M.
T.M., Kerlavage A.R., A
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EMBL; AC004005; AAC23405.2; -.
EMBL; AF332565; AAK06847.1; -.
EMBL; AY056238; AAL07087.1; -.
EMBL; AF375410; AAK52994.1; -.
EMBL; AF367277; AAK56266.1; -.
EMBL; AY129474; AAM91060.1; -.
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Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann (
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Naruse
Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakaroh H., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K
Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis cDNA clones.";
Submitted (May-2007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv.
Town C.D.,
Submitted (
Pfam; PF05383; La; 1.
PRINTS; PR00302; LUPUS
Hypothetical protein.
SEQUENCE 545 AA; 60
                                                                                                                                                                                                                                            Shinn P. Chen H., Cheuk R., Kim C.J., Banh J., Bowser L., Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S. Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis ORF clones.", Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowser L., Carninci P., Cheuk R., Kim C.J., Meyers M.C., Banh J., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Southwick A., Toriuni M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis cDNA clones."; "Arabidopsis cDNA clones."; "Jubmitted (MAR-2001) ---"
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"Arabidopsis thaliana
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                                                                                               GO; GO:0005634; C:nucleus; IEA
GO; GO:0003723; F:RNA binding;
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ch H.L., Tang C., Toriumi M.,
Carninci P., Chen H., Cheuk F
T., Kamiya A., Karlin-Neumann
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 E1A933261FE1ED80 CRC64;
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n H., Cheuk R., Hayashizaki
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SEQUENCE FROM N.A.
STRAIN=Reynolds and Newman;
MEDLINE=97388587; PubMed=9245821;
Sau S., Bhasin N., Wann E.R., Lee J.C., Foster
"The Staphylococcus aureus allelic genetic lor
"The Staphylococcus aureus allelic genetic lor
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SEQUENCE FROM N. STRAIN=Reynolds
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STRAIN=Reynolds and Newman;
MEDLINE=98125727; PubMed=9466251;
                                                                                                                                                                                                                                                             "Staphylococcus aureus cap50 and cap5P genes functionally complement mutations affecting enterobacterial common-antigen biosynthesis in Escherichia coli.";
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Pfam; PF02350; Epimerase 2; 1.
TIGRPAMs; TUGR00236; weeB; 1.
SEQUENCE 391 AA; 44247 MW;
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HSSP; P27828;
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J. Bacteriol. 179:1614-1621(1997).
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STRAIN=Becker;
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                                                             Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee "Identification of a gene essential for O-acetylation of the Staphylococcus aureus type 5 capsular polysaccharide.", Mol. Microbiol. 27:9-21(1998).
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P; P27828; 1F6.

G0:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;

G0:0009103; P:lipopolysaccharide biosynthesis; IEA.

G0:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bagga N., Wann E.R., Foster T.J., Lee J.C.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ EMBL; U81973; AAC46099.1; -
HSSP; P27828; 1F6D.
GO; GO:0008761; F:UDP-N-acetylglucosamine 2-ep:
GO; GO:0009103; P:lipopolysaccharide biosynthes
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Q99X57;
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Bacteria; Firmicutes; Bacillales; S
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EMBL; AP003358; EAB56326.1;
EMBL; AP003129; EAB41379.1;
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                                                                                                                                      GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; GO:0009103; P:Lipopolysaccharide biosynthesis; IEA. GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA. erPro; IPR003331; Epimerase 2. m; PF02350; Epimerase 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; GO:0009103; P:lipopolysaccharide biosynthesis; IEA. GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
362
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PF02350; Epimerase 2: 1.
AMB; TIGR00236; wecB; 1.
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QASRRICEAIEYYFG
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                                                                                                   44372 MW;
                                                           51.0%;
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376
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Last annotation updat
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Pred. No.
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Pred. No. 2.
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01-JUN-2003
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Q8T8V5;
01-JUN-2002
01-JUN-2002
01-OCT-2003
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                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to sjogren syndrome antigen B (Autoantigen Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                  Submitted (JAN-2002) to the EMBL/Ge
EMBL; AY075257; AAL68124.1; -.
FlyBase; FB9R0011638; La.
GO; GO:0008098; F:5S rRNA primary t
GO; GO:0003723; F:RNA binding; NAS
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; SEQUENCE 401 AA; 46138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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Cyprinidae; Danio.
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                                                                                                                                                                                                       Patel S., Pho
Celniker S.;
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LA OR CG10922
                InterPro; IPR002344; Lupus_La_dom
InterPro; IPR006630; Lupus_La_dom
InterPro; IPR000504; RNA_rec_mot.
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SM00715; LA; 1.
SM00360; RRM; 1.
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Pred. No.
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PRINTS; PR00302; LUDUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS00102; RRM; 1.
PROSITE; PS00103; RRM; RNP 1; 1.
SEQUENCE 390 AA; 44869 MW;
                                                                                                                                                                                                P72382;
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SEQUENCE
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Lancet 359:1819'1827(2002).

EMBL, AP004822; BAB94004.1; .

GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;

GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.

GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.

InterPro; IPR003331; Epimerase_2.
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                                                                                                                            Cap8P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; BNYNB
MEDLINE=96178981;
                SEQUENCE FROM N.A. STRAIN=Becker;
                                                                 Bacteria; Firmic
NCBI_TaxID=1280;
                                                                                      Staphylococcus aureus Bacteria; Firmicutes;
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01-JUN-2003
                                                                                                                                                                                                                                       P72382
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Baba T., Takeuchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i.
; PubMed=12044378;
; Kuroda M., Yuzawa H
Naimi T., F
PubMed=8606192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (strain MW2)
Bacillales;
                                                                                        Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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24, Last a
synthesis
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Last annotation update)
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Pred. No.
                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB Pred. No. 2.9; 1; Mismatches
                                                                                                                                                                                                                                       PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125E4D5D1904779C CRC64;
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                                                                                                                                                                annotation update)
                                                                                                                                                                                     sequence update)
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Kuroda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 381;
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RESULT
OR BTU4
AC Q8
AC 
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Q7ZTK2
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Best Local S
Matches 15
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Best Local Similarity
Matches 15; Conserv
Q7ZTK2
Q7ZTK2;
01-JUN-2003
01-JUN-2003
01-OCT-2003
Similar to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8BTU4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006530; Lupus La dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Ppfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sjogren syndrome antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SEQUENCE 381 AA; 43891
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
SEQUENCE 415 AA; 47657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRALN-NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK088677; BAC4
MGD; MGI:98423; SBb.
GO; GO:0005634; C:nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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(TrEMBLrel. 23,
(TrEMBLrel. 25,
drome antigen B.
  lupus LA protein
                        (TrEMBLrel. (TrEMBLrel.
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                                                                  (TrEMBLrel.
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                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                          85.3%;
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                        224,
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                                                                                                                                                                                                                                                                                                                          Score 87; Pred. No.
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Last annotation update)
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                        Last sequence update)
                                                                Created)
  homolog
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                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                        A7545C7686AC8363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2E2DEF1452C0F0E9 CRC64;
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5.7e-06;
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annotation
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RESULT 4
RESULT 4
RECHIEF
ID 080H
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Best Local Similarity
Matches 11; Conserv
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PRINTS; PR0302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 1.
SEQUENCE 427 AA; 48996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8QHI5
Q8QHI5;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

LYECUYEY T.J., Fang H.-L.;

LYECUYEY T.J., Fang H.-L.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AP467897; AAL76289.1; -.

GO; GO:0005534; C:nucleus; IEA.

GO; GO:0003733; F:RNA binding; IEA.

InterPro; IPR00244; Lupus La.

InterPro; IPR006630; Lupus La.

InterPro; IPR006630; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMB!
EMBL, BC046654; AAH46654.1; -.
GO; GC:0005534; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_7
                                                                                                                                              PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; SEQUENCE 206 AA; 23992 MW;
                                                                                                                                                                                                                  PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25, Untranslated region binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                        Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La dom.
InterPro; IPR00504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue=Embryo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TaxID=9031;
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                                                  11;
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  4 EAKICHQIEYYFGD
                                                                        Similarity
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48996
                                                                      63.7%;
78.6%;
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78.6%;
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                                               ; Score 65; DB
; Pred. No. 0.01
2; Mismatches
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Last annotation update)
-protein.
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                                                                                                 DB 13;
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                                                                                            Length 206;
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47

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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: sp_archea:*
2: sp_bacteria:*
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4: sp_human:*
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137.751 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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102
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: sp_invertebrate:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	თ	ហ	4	w	2	ш	Result No.
47	47.5	48	48	48	50	52	52	52	52	57	58	65	66	87	87	Score
46.1	46.6	47.1	47.1	47.1	49.0	51.0	51.0	51.0	51.0	55.9	56.9	63.7	64.7	85.3	85.3	Query Match Length
396	329	2349	756	545	91	391	391	391	381	390	401	206	427	415	381	Length [
v	16	ហ	16	10	ហ	16	N	N	16	თ	13	13	13	11	1	DB
001806	Q87T57	Q81455	Q8A8Y5	080567	044678	Q99X57	P95709	P72382	BNANBÖ	Q8T8V5	Q7ZTI0	Q8QHI5	Q7ZTK2	Q8BTU4	Q9СҮВ9	IJ
001806 caenorhabdi	Q87t57 vibrio para	Q8i455 plasmodium	Q8a8y5 bacteroides	O80567 arabidopsis	O44678 caenorhabdi	Q99x57 staphylococ	P95709 staphylococ	P72382 staphylococ	Q8nyn8 staphylococ	Q8t8v5 drosophila	Q7zti0 brachydanio			O8btu4 mus musculu	Q9cyb9 mus musculu	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
43	43	43	43	43.5	43.5	43.5	43.5	44	44	44	44	44	44	44.5	44.5	45	45	45	45	45	45	45	46	46	47	47	47	47
•		٠	42.2	42.6	42.6				43.1	43.1	•	•	43.1		43.6	44.1	44.1	44.1	44.1	•	44.1		45.1	•	•		46.1	46.1
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	Q9ngg5 drosophila		neurotheca		escherichi			י ס		Q7y1el oryza sativ	drosophila	Q8t907 drosophila	Q9aug1 brassica ol	oryza sati	rhodop	α				. 7	Q8lmp9 oryza sativ	anabae	bacillus h	vibrio pa	oryza	Vibrio	arabid	9

ALIGNMENTS

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SEQUENCE PROM N.A. STRAIN-C57BL/6J; TISSUE=Embryo; MEDLINE-21085660; PubMed=11217851; Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kasukawa T., Saito R., Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washi K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., "Functional annotation of a full-length mouse cDNA collection."; MGD; MGI:98423; Ssb.	THT 1 (B9 (B9) (B9) (PELIMINARY; PRT; 381 AA. (9CYB9) (1-JUN-2001 (TrEMBLrel. 17, Created) (1-JUN-2001 (TrEMBLrel. 17, Last sequence update) (1-OCT-2003 (TrEMBLrel. 25, Last annotation update) (1-Sjogren syndrome antigen B. (Sjogren syndrome antigen B. (SB. SB. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus. (11) (11)

MEDLINE=22388257; PubMed=12477932;

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gav L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gav L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gav L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimsood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimsood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimsood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimsood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimsood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimsood J., Schmutz J.M.,
RA Rodriguez A.
                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
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Pfam; PF00097; zf-C3HC4; 1.
PRINTS; PR01406; BBOXZIPINGER.
SMART; SM00336; BBOX; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00188; PRY; 1.
SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
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Zinc-finger;
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EMBL; AP00051; BAB63330.1; --
EMBL; BC024039; AAH24039.1; --
EMBL; BC032297; AAH32297.1; --
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GO; GO:0003677; F:DNA binding; TAS.
GO; GO:0005515; F:protein binding; TAS.
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InterPro; IPR006574; PRY.
InterPro; IPR003877; SPRY receptor.
InterPro; IPR00315; Znf_Bbox.
InterPro; IPR001841; Znf_ring.
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   95
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E; PS00518; ZF RING 1; PJ

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G 97 138 RI

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18
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EQQDAKLCERHREKLHYYCED 115
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97
188
365
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422
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539 AA;
                                                                                                                           Conservative
                                                                                                                                                      40.2%;
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                                                                                                                        ; Score 41; DB; Pred. No. 34; 5; Mismatches
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POLY-GLU.
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Search completed: September 10, 2004, 17:53:04 Job time: 8.24022 secs
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Best Local
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SEQUENCE FROM N.A.
MEDLINE=91373339; PubMed=1894617;
MEDLINE=91373339; PubMed=1894617;
Brigle K.E., Westin E.H., Houghton M.T.,
"Characterization of two cDNAs encoding;"
"Characterization of two cDNAs encoding;"
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994
01-JUN-1994
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.
STRAIN=NUB36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Amino-acid transport; Transport; Membrane; ATP-binding
Amino-acid transport; Transport; Membrane; ATP-binding
AMIP_BIND 34 41 ATP (BY SIMILARITY)
  MEDLINE=94140851;
Brigle K.E., Seit
"Increased expres
                                                                                                                     genomic
                                                                                                                           L1210 murine leukemia cells.
genomic rearrangement.";
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                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                     Biol.
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. Chem. 266:17243-17249(1991).
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(Rel. 29, Last sequence update)
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her R.L., Westin
sion and genomic
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2; Mismatches
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Sciurognathi; Muridae;
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  E.H., Goldman organization
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\begin{array}{c} R_1 \\ R_2 \\ R_3 \\ R_4 \\ R_4 \\ R_5 \\
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Best Local :
                                                              SEQUENCE FROM N.... Shiina S., Tamiya G., C
Shiina S., Tamiya G., C
"Homo sapiens 2,229,81"
"----mitted (SEP-1999) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _HUMAN
Z173_HUT
Q12899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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-i- FUNCTION: Binds to folate and reduced folic acid mediates delivery of 5-methyltetrahydrofolate to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=96079113; PubMed=8530076;

Chu T.W., Capossela A., Coleman R
"Cloning of a new 'finger' protein
region of the human MHC.";

Genomics 29:229-239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
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TRIM26 OR ZNF173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Zinc finger protein 173 (Tripartite mo
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SEQUENCE FROM N.A TISSUE-Brain, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
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MGI:95569; Folr2.
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PP03024; Folate_rec; 1.

ptor; Glycoprotein; Signal; Placenta; lytor; Glycoprotein.

anchor; Multigene family; Lipoprotein.

POTENTIAL.

POTENTIAL.
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L25338; AAA37594.1;
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Belongs to the folate receptor
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                                                                                          ., Inoko H.;
enomic DNA of 6p21.3 HLA cla
EMBL/GenBank/DDBJ databases
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N-LINKED (GLCNAC. . .)
; 8404EACEB1BFECC7 CRC6
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REMOVED IN MATURE FORM (POTENTIAL)
GPI-anchor amidated Berine (Potent
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Catarrhini; Hominidae;
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motif-containing
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(By similarity)

SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.

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Bioinformatics

and the

EMBL outstation a collaboration FUNCTION: PARTICIPATES IN THE EFFLUX OF AMINOGLYCOSIDES. CONFERS RESISTANCE TO A VARIETY OF THESE SUBSTANCES. SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane

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RESULT 12
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                                                          Query Match
Best Local S
Matches 10
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EMBL; U10436; AAA74741.1; -.
EMBL; AE000334; AAC75523.1; -.
EMBL; D90875; BAA16344.1; -.
EMBL; D90876; BAA16348.1; -.
EMBL; D90876; BAA16348.1; -.
EMBL; M59403; CAA40663.1; -.
EMBL; X57403; CAA40663.1; -.
PIR; E65072; E65022
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InterPro; IPR004764; HAE1.
Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
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                                                           Conservative
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                                                                                            113047
                                                                                                   11 (BY SIMILARITY).

PERLPLASMIC (BY SIMILARITY).

12 (BY SIMILARITY).

12 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

A -> G (IN REF. 1).

A -> D (IN REF. 1).

C -> PD (IN REF. 1).
                                                                   Score 43.5;
Pred. No. 26;
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CYTOPLASMIC (BY SIMILARITY).
1 (BY SIMILARITY).
PERIPLASMIC (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
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RIPLASMIC (BY S
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RESULT 13
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Matches 6
                                                                                   01-AUG-1992
01-AUG-1992
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                         Meiosis; I
Nuclease;
SEQUENCE
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacill
NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sekelsky J.J., McKim K.S., Chin G.M., Hawley R.S.;
"The Drosophila meiotic recombination gene mei-9 encodes a homologue
of the yeast excision repair protein Radl.";
Genetics 141:619-627(1995).
-i- FUNCTION: Implicated in recombination events during meiosis,
mostly in meiotic exchange. May directly resolve Holliday
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEI9_DROME
Q24087;
                                                      Glutamine transport ATP-binding GLNQ.
                                                                                                                                                    GLNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U27181; AAC46917.1; -. PIR; S58936; S58936. FlyBase; FBgn0002707; mei-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02732; ERCC4; 1.
TIGRRAMS; TIGR00596; rad1; 1.
Meiosis; DNA repair; DNA-binding; Nuclear protein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GG; GO:0007059; P:chromosome segregation; IMP. GO; GO:0007131; P:meiotic recombination; IMP. GO; GO:0006298; P:mismatch repair; IMP. GO; GO:0006289; P:nucleotide-excision repair; IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hoxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DROME
                                                                                                                                   P27675;
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InterPro; IPR006167; Rad 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96109608; PubMed=8647398; Sekelsky J.J., McKim K.S., Chin G.M., "The Drosophila meiotic recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEI-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mei-9 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      junctions within recombination intermediates leading to DNA exchange. Also required for the repair of mismatches within meiotic heteroduplex DNA and for nucleotide excision repair. SUBUNIT: Heterodimer (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: Belongs to the XPF family.
                                                                                                                                                    BACST
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                                                                                                                                                                                                                                                             QEAKICHQIEYY 14
                                                                                                                                                                                                                                                                                                                                                                          Endonuclease.
                                                                                                                                                                                                                                                                                                                                                           926 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                         105685 MW;
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50.0%;
                        Bacillales; Bacillaceae; Geobacillus
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                                                                                                                                                                                                                                                                                                           Score 43; DB
Pred. No. 28;
                                                                     protein glnQ
                                                                                                                                                                                                                                                                                                                                                           342C2C91BB3AFD91 CRC64;
                                                                                                                                                    242 AA
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T43542; T43542

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SMART; SM00715; LA; 1.

SMART; SM00305; RRM; 1.

SMO350; RRM; 1.

PROSITE; PS00030; RRM RNP 1; FALSE_NEG.

RNA-binding; Nuclear protein.

RNA-binding; Nuclear protein.

RNA-binding; Nuclear protein.

COMPLICT 188 188 M -> I (IN F
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InterPro; IPR002344; Lupus_La_
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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15-DEC-1998
10-OCT-2003
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Logemann E., Parniske M., Hahlbrock K.;
"Modes of expression and common structural features of the phenylalanine ammonia-lyase gene family in parsley.";
Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995).
-!- FUNCTION: Controls carbon flux to pigments essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid
4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000504; Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-hydroxylase) (CA
CYP73A10 OR CYP73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                EMBL; L38898; AAC41660.1; -.
PIR; T14907; T19907.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95320184; PubMed=7597051;
Oxidoreductase; Monooxygenase; Heme; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Lignin biosynthesis.
PATHWAY: Phenylpropanoid metabolism; second step.
SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pollination or UV protection, to numerous pytoalexins synthesized by plants when challenged by pathogens, and to lignins. CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-hydroxycinnamate + NADP(+) + H(2)O.
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                            PR00385; P450.
; PS00086; CYTOCHROME_P450; 1.
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298 AA;
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Pred. No. 2.6;
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64E6AB99940B87F4 CRC64;
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P24177; P76971; P77178; C

01-MAR-1992 (Rel. 21, Crec

01-NOV-1997 (Rel. 35, Lag

16-OCT-2001 (Rel. 40, Lag
                                                                                                                                                                                                      MEDLINE=97349980; PubMed=9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kinura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satch Y., Sivasundaram S.
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.
Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                           Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose L Mau B., Shao Y.;
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Submitted (AUG-1995) to th
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ma D., Cook D.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
Enterobacteriaceae; Eschei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
  Rosenberg E.Y., Ma D., Nikaido H.; "AcrD of Escherichia coli is an aminoglycoside J. Bacteriol. 182:1754-1756(2000).
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=K12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable aminoglycoside efflux pump
                                  MEDLINE=20158894;
                                                                              "Cloning, character
Escherichia coli."
                                                                                        Bouvier J., Richaud C., Higg
"Cloning, characterization,
                                                                                                               MEDLINE=92355499; PubMed=1644752;
                                                                                                                                                                     "Construction of a contiguous 874-kb (K12 genome corresponding to 50.0-68 analysis of its sequence features.";
                                                                                                                                                                                                                                                                                      STRAIN=K12;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      Science
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                                                                    Bacteriol.
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nce 277:1453-1474(1997).
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SEQUENCE
                                                                                                                                          Pardigon N., Strauss J.H.;
"Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";
J. Virol. 70:1173-1181(1996).
-I- FUNCTION: May be involved in transcription termination by RNA polymerase III. Binds RNA and DNA. Binds to the 3' end of the minus strand of Sindbis virus RNA. This may be significant for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q26457;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                        PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
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InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
SIMILARITY: TO VERTEBRATE PROTEIN LA.
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SUBCELLULAR LOCATION: Nuclear. Primarily nuclear,
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RA Later 415:871-880(2002).
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TIAHI SCHPO STANDARD; PRT; 298 AA.
P87058; 013362; Q10458;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La SLAI OR SPACS7A10.10C.
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                                                                   EMBL;
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Binds to the precursors of polymerase III RNAs.
FUNCTIONS in tRNA maturation.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
-!- SIMILARITY: TO VERTEBRATE PROTEIN LA.
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Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jtsumi R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                              AB011371; BAA24981.:
Z94864; CAB08173.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                          noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoantigen homolog).
                                                                                                                                                                                                                                                                                                                                restrictions
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                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                     collaboration -
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Query Match
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SMART; SM00715
SMART; SM0036(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50102; RRM; 1. 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; P
DOMAIN 111 203 RN
MEDLINE-2019606; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P40796; Q24375; Q9YIN2;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                           growth
                                                                                                                                                                                                         "La proteins from cerevisiae: a year
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=94309661;
                                                                                                                                                                                                                                                                                                                                  Bai C., Li Z., Tolias P.P.;
"Developmental characterization of a Drosophila RNA-binding pro
homologous to the human systemic lupus erythematosus-associated
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Canton-S; TISSUE=Ovary; MEDLINE=94309632; PubMed=8035794;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             La protein homolog (La ribonucleoprotein) (La LA OR CG10922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                     La/SS-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002344;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Yoo C.J., Wolin S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S33818; S33818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X68817; CAA48715.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR00302; LUPUSLA.
                                                                                                                                                                                                                                                                                                        autoantigen.";
ll. Biol. 14:5123-5129(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                  FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTKICEQIEYYFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAKICHQIEYYFGD
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IPR000504;
                                                                                                                                                                              Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; LA; 1.
60; RRM; 1.
                                                                                                                                                                                                        from Drosophila melanogaster and Saccharomyces yeast homolog of the La autoantigen is dispens
                                                                                                                                                                                                                                                                                                                                                                                                                  N.A
                                                                                                                                                                              14:5412-5424(1994).
                                                                                                                                                                                                                                                         PubMed=8035818;
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332
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Lupus_La_dom.
RNA_rec_mot.
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78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Phosphorylation.
RNA-BINDING (RRM).
NUCLEAR LOCALIZATION SIGNAL
NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 1;
Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB3A38B7D2E3EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                             dispensable
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Mays A.D., Dew I., Dietz S.M.,
RA Cholson K., Doup L.E., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Roccha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., France C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Melson D.L.,
RA Mont S.M., Nelson K.A., Nixon K., Nusskern D.R., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Samders R.D.C., Scheler F., Shen H.,
RA Rainert K., Semington K., Samders R.D.C., Scheler F., Shen H.,
RA Rainert K., Semington K., Samders R.D.C., Scheler F., Shen H.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier B., Spradling A.C., Tanger S., Van S., Tang S., Yao Q.A.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Kimmel B.E., Schen S., Langer R., Venter E., Wang S., Yao Q.A.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Mang Z.-Y., Wassarman D.A., Weinsche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear (Probable).

DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo followed by a restricted pattern of mesodermal expression that later confined to the visceral mesoderm, gonads, gut, and salivers that the confined to the visceral mesoderm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glands.
SIMILARITY: Contains 1 RNA recognition
SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    motif (RRM) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and salivary
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entities or send a modified the between s SWISS-PROT entry is copyright. It is produced through a c ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and fo ities requires a license agreement (See http://www.isb-sibs requires a license agreement (Se an email to license@isb-sib.ch). restrictions tent is in is for a collaboration ch/announce/ 8

Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
Pfam; PF00076; rrm; 1.
PRINTS; PR00302; LUPUSLA.
-SMART; SM00715; LA; 1.
SMART; SM00716; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM; NRP 1; 1.
PROSITE; PS00030; RRM RNP 1; 1. DOMAIN CONFLICT EMBL; U07652; AAA20518.1; -EMBL; L32988; AAA21776.1; -EMBL; AE003666; AAP53885.1;
PIR; A53773; A53773.
PIR; A53781; A53781. InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot. Base; FBgn0011638; La. GO:0008098; F:5S rRNA primary t GO:0003723; F:RNA binding; NAS . ; DNA-binding.
RNA-BINDING (RRM)
A -> T (IN REF. 1 transcript binding; (IN REF. 1) IDA

gh a collaboration -EMBL outstation -

outstation

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RESULT 5
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Best Local S
Matches 1:5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992
01-AUG-1992
15-MAR-2004
This SWI
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93287095; PubMed=8510143;
Scherly D., Stutz F., Lin-Marq N., Clarkson S.G
"La proteins from Xenopus laevis. cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAB_XENLA
P28049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; P
DOMAIN 111 187 RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comenties requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; J
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                           expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAB1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC1494; JC1494.
InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (enopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nomolog B).
                                          embryos.

PTM: Phosphorylated (Probable).

MISCELLANEOUS: There are two forms of La, LaA and LaB, in SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.

SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                     FUNCTION: La protein plays a role in the transcription of RNA polymerase II. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).

SUBCELLULAR LOCATION: Nuclear (Probable).

DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly
                                                                                                                                                                      constant steady state level
                   SWISS-PROT entry is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                            Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100
LS; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAKICHQIEYYFGDF
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415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 43, Last annotation update)
otein homolog B (La ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus.
                                                                                                                                                                                                                                                                                                                                          231:196-204(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
ry is copyright. It is produced through a collaboration Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47777 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Phosphorylation.
RNA-BINDING (RRM).
; 033FD9CC1E475F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                      in mature
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; Pipidae;
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TABA XENIA SIATULA
P28048;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last ser
15-MAR-2004 (Rel. 43, Last an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENLA
                                                                                                                                                                                                            This
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                              Scherly D., Stutz F., Lin-Marq N., "La proteins from Xenopus laevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X68818; CAA48716.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93287095; PubMed=8510143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05383; La; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nomolog A).
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                                                                                                   embryos.

PTM: Phosphorylated (Probable).

PTM: Phosphorylated (Probable).

MISCELLANEOUS: There are two forms of La, LaA and LaB, in SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.

SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S33817; S33817
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IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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315
427 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (African clawed frog).
azoa; Chordata; Craniata; Vertebrata; I
achia; Anura; Mesobatrachia; Pipoidea;
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78.6%;
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: annotation
(La ribonuc
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Pred. No.
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NUCLEAR LOCALIZATION
; 45F3146F8934A355 CI
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ribonucleoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                       , Clarkson S.G.; cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                       in xenopus
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                                                                                                                                                                                                                                                                                                 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., William P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
Thuman and mouse cDNA sequences.;
Thuman and mouse cDNA sequences.;
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01-OCT-1993
01-OCT-1993
15-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=93203630; PubMed=8454877;
Topfer F., Gordon T., McCluskey J.;
TCharacterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and of conserved RNA-binding motifs, with poly(U) and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclear protein.
DOMAIN 111
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                                                                                                                                                               Groelz D., Bachmann M.;
Submitted (OCT-1996) to the
                                                                                                                                                                                                                               SEQUENCE OF 1-11 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
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                               PUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.55, 55, 75
  polymerase III tra
of RNA polymerase
and 7-2 RNAs.
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Last annotation update)
                                                                                                                                                                                                                                                                                         U.S.A.
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; EC153C15F9187FC4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                         99:16899-16903 (2002)
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5.4e-07;
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Best Local
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                              "Isolation of rat cDNA clones coding for the autoantigen SS-B/La: detection of species-specific variations.";

Gene 126:265-268(1993).

-I- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use
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PROSITE; PS00030; RRM RNP_1; 1.

RNA-binding; Nuclear protein; Phosphorylation.

DOMAIN 111 187 RNA-BINDING (RRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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\frac{1}{1} \cdot \frac{1}{1} \cdot \frac{1}{1}
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=93246255;
                                                                                                                                                                                                                                                                                                                                                                                     NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homolog)
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InterPro; IPR006630;
                                                                                                                                                                                                                                                                             Bachmann M.;
                                                                                                                                                                                                                                                                                                   Semsei I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lupus La protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005634; C:nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                 SUBUNIT: Interacts with DDX15
SUBCELLULAR LOCATION: Nuclear
PTM: Phosphoryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
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PTM: Phosphorylated SIMILARITY: Contains
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                                                                                                                                                                                                                                                                                                                                                                                _TaxID=10116;
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Y07951; CAA69249.1; -.
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homolog
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31,
                                                                                                                                                                                                                                                                                               PubMed=7916708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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100.0%;
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RNA_rec_mot.
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Sciurognathi; Muridae
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recognition motif (RRM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                               Muridae;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoantigen
                                                                                                           n precursor forms and 4.5S, 5S, 7S,
                                                                                                                                                                                                                                                                                                        G.L.,
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Raba G.M., Hong L.,
A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
A Hopkins R.F., Jordan H., Moore T., Karninci P., Frange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,
A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hokesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89202037; PubMed=2468131;
Chan E.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
sequences for RNA-binding.";
Nucleic Acids Res. 17:2233-2244(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P05455;
01-NOV-1988 (Rel. 09, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Lupus La protein (Sjogren syndrome type B ant
ribonucleoprotein) (La autoantigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
La. "
(5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89053970; PubMed=3192525; Chambers J.C., Kenan D., Martin B "Genomic structure and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                            SEQUENCE OF 54-408 FROM N.A.
MEDLINE=88199081; PubMed=2452201;
Sturgess A.D., Peterson M.G., McN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                Sturgess A.D., Coppel R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta, a
MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Che
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                                                  "Characteristics
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#UNCLINE.89251617; PubMed=2470550,
MEDLINE-89251617; PubMed=2470550,
Gottlieb E., Steitz J.A.;
"Function of the mammalian La protein: evidence for "Function of the mammalian by RNA polymerase III.";
PROSITE;
             PRINTS; PR00302; LUPUS
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1
                                                                                                                                                          888
                                                                                                                                                                                                                                                      EMBL; J04205; AAA51885.1; --
EMBL; BC001289; AAH01289.1;
EMBL; BC020818; AAH20818.1;
PIR; A31888; A31888.
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-I- FUNCTION: La protein plays a role in the transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97207017; PubMed=9054510; Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Maraie R.J.; "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes."; Cell 88:707-715(1997).
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MEDLINE=85166283; PubMed=3856888;
Chambers J.C., Keene J.D.;
"Isolation and analysis of cDNA c
                                                            Pfam; PF05383; La; Pfam; PF00076; rrm
                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                              [nterPro;
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SUBUNIT: Interacts with DDX15.
SUBUNIT: Interacts with DDX15.
SUBCELLULAR LOCATION: Nuclear (Probable).
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
PTM: The N-terminus is blocked.
DISEASE: Sera from patients with systemic lupus erythematosus often contain antibodies that react with the normal cellular La protein as if this antigen was foreign.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                        GO:0030529; C:ribonucleoprotein complex
GO:0003729; F:mRNA binding; TAS.
GO:0000049; F:tRNA binding; TAS.
GO:0008334; P:histone mRNA metabolism;
GO:0008334; P:tRNA modification; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription terminatifactor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor fof RNA polymerase III transcripts including tRNA and 4.5S, 5S
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                                                                                                                                                                                                                                                                                                                                                                                      non-profit institutions as long and this statement is not removed.
                                                                                       IPR002344; Lupus_La.
IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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A31986.1; B449; Lupus B449; Lupus B449; Lupus B504; RNA_ri a; 1. TM; 1. LUPUSLA. LLA; 1. ; RRM; 1. ; RRM; 1. ; RRM; 1.	act for try	SEQUENCE FROM N.A. TISSUB-Pituitary; MEDLINE-99202037; PubMed-2468131 Chan E.K.L., Sullivan K.F., Tan "Ribonucleoprotein SS-B/La belon sequences for RNA-binding."; Nucleic Acids Res. 17:2233-2244 -!- FUNCTION: La protein plays a polymerase III transcripts. of RNA polymerase III transcripts.	11, Creat 11, Last 41, Last 41, Last 10molog () 1, Chorda 1, Cetart Bos.		482 488 507 755 7209 1070 200 200 281 394 416
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hypothetical protein alr4821 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2408
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, SDNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium AnalyReference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2408
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: H83743
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-642 <STO>
A;Cross-references: GB:AP001509; GB:BA0000004; NID:gl0173176; PIDN:BAB04471.1; GSPDB:GN00A; Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76520.1; PID:g17133958; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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Search completed: September 10, 2004, 18:02:28 Job time: 15.0782 secs
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-529 < ROU>
A; Cross-references: EMBL: AC004005; NID: g3212846; PID: g3212854
A; Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I; Town, C.D.; Fujii, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Taleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
A; Accession: G84872
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N;Alternate names: hypothetical protein F6EI3.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00677; G84872
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F6EI3 genomic sequence.
A;Reference number: Z14180
A;Accession: T00677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C44B4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T30953
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A;Molecule type: DNA
A;Residues: 1-396 <SAM5
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A;Gene: F6El3.10; At2g43970
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Best Local
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Note: C44E4.4
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8; Conserv
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RESULT 13
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C;Accession: T38937
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A;Cross-references: EMBL:Z94864; PIDN:CAB08173.1; GSPDB:GN00066; SPDB:SPAC57A10.10c
A;Experimental source: strain 972h-; cosmid c57A10
                                                                                                                                               A;Description: the binding of the La protein to tRNA precursors C;Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, February 1998
A;Description: Screening of S. pombe cDNA library using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Van Horn, D.J.; Yoo, C.J.; Xue, D.; Shi, H.; Wolin, RNA 3, 1434-1443, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-binding protein La1 homolog - fission yeast (Schizosaccharomyces N_iAlternate names: La autoantigen; ribonucleoprotein La homolog
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A; Introns: 72/1
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A; Residues: 1-298 <UTS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: The La protein in Schizosaccharomyces pombe: a A; Reference number: Z22560; MUID:98067398; PMID:9404894
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:Residues: 1-298 <VAN>
                                                                                         Query Match
Best Local
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(permease) BH0752 [imported] - Bacillus halodurans (strain C-125)

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A;Cross-references: EMBL:X68817; NID:g64873; PIDN:CAAA8715.1; PID:g64874 C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology F;112-178/Domain: ribonucleoprotein repeat homology F;113-118/Region: RNA-binding RNP2 motif F;151-158/Region: RNA-binding RNP1 motif F;151-158/Region: RNA-binding RNP1 motif F;1228-428/Domain: phosphory/larcal matrix
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J. Mol. Biol. 231, 196-204, 1993
A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33818
A;Accession: S33818
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:X68817; NID:964873; PIDN:CAA48715.1; PID:964874
A;Cross-references: EMBL:X68817; NID:964873; PIDN:CAA48715.1; PID:964874
C;Comment: This protein associates with a variety of small RNA molecules, most of wh
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein
C;Keywords: leucine zipper; RNA binding
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Mol. Cell. Biol. 14, 5123-5129, 1994
A;Title: Developmental characterization of a Drosophila RNA-binding
A;Reference number: A53773; MUID:94309632; PMID:8035794
A;Reference number: A53773;
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              A;Molecule type: mRNA
A;Residues: 1-390 <YOO>
A;Cross-references: GB:L32988;
C;Genetics:
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R;YOO, C.J.; Wollin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanc
A;Reference number: A53781; MUID:94309661;
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A; Residues: 1-390 <BAI>
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A;Status: preliminary
                                                                                                                                                                                                                                                                                             ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
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;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change
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Date: 13-Jan-1995 #sequence_revision
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FlyBase:La
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A;Cross-references: FlyBase:FBgn0011638
C;Superfamily: ribonucleoprotein La; rik
C;Keywords: RNA binding
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89777
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
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A;Nolecule type: DNA
A;Residues: 1-166 <DAV>
A;Cross-references: EMBL:AF039051; PIDN:AAB94258.1; GSPDB:GN00023; CESP:C14C6.12
                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid C14 A;Re: erence number: 221210 A;Ar.aeri- manager: 221210
                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C14C6.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change
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A;Experimental source: strain N315
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A; Residues: 1-391 < KUR>
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10; Conservative
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QQEAKICHQIEYYFGDF 18
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62.5%;
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60.0%;
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58.8%;
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Pred. No.
                                      Score 50; DB 2;
Pred. No. 0.83;
1; Mismatches
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Pred. No. 0.91;
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A;Cross references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457 R;KOhsaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka, J. Clin. Invest. 85, 1566-1574, 190 A;Title: Fine epitope mapping the human SS-B/La protein: Identification of A;Reference number: I55553; MUID:90237237; PMID:1692037 A;Accession: I55553
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A;Molecule type: mRNA
A;Residues: 1-19, "E',21-47 <NYM>
R;Sturgess, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham,
J. Immunol. 140, 3212-3218, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: this sequence has been revised in reference A31888 R;Nyman, U.; Ringertz, N.R.; Pettersson, I. Immunol. Lett. 22, 65-7, 1989 A;Title: Demonstration of an amino terminal La epitope recognized by A;Reference number: A61051; MUID:89379261; PMID:2476379 A;Accession: A61051
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDNA clones expressing human
A;Reference number: A22956; MUID:85166283; PMID:3856888
A;Accession: A22956
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A; Residues: 174-224 < RE2 >
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A;Accession: I70205
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A;Accession: SO3848
A;Molecule type: mRNA
A;Residues: 1-408 <CH2>
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A;Residues: 45-97,'LK' <CH3>
A;Cross-references: GB:J04205
                                                                                                                                                                                                                  Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                      Superfamily: ribonucleoprotein La, ribonucleoprotein repeat Reywords: phosphoprotein; RNA binding; 112-178/Domain: ribonucleoprotein repeat homology <RRM>;113-118/Region: RNA-binding RNP2 motif; 113-158/Region: RNA-binding RNP1 motif; 151-158/Region: RNA-binding RNP1 motif; 151-158/Region: RNA-binding RNP1 motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Gene: GDB:SSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:M35263; NID:g338492; PIDN:AAA36653.1; PID:g338496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GDB:125359; OMIM:109090
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                                                                                                                                                       EAKICHQIEYYFGDF
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                                                                                                                                                                                                                                           85.3%; Score 87; DB 1; 100.0%; Pred. No. 1.7e-
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ribonucleoprotein La.A - African clawed frog
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: S33818; S28545
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S33818

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C;Date: 03-Feb-1994 #sequence revision 26-May-1994 #text C;Accession: S33817; S28544
R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G. J. Mol. Biol. 231, 196-204, 1993
A;Title: La proteins from Xenopus laevis. cDNA cloning a A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33817
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S33817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: C; Species: Xenopus
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(Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

(Keywords: phosphoprotein; RNA binding

F;112-178/Domain: ribonucleoprotein repeat homology <RRM>

F;113-118/Region: RNA-binding RNP2 motif

F;151-158/Region: RNA-binding RNP1 motif
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A;Experimental source: liver
C;Comment: This protein associates with a variety of small RNA molecules,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-427 < SCH>
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A; Residues: 1-415 < SEM>
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RESULT 5
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                        ;Keywords: phosphoprotein; RNA binding;111-17/Domain: ribonucleoprotein repeat;112-117/Region: RNA-binding RNP2 motif;150-157/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                         Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternate names: autoantigen SS-B/La; ribonucleoprotein; Species: Xenopus laevis (African clawed frog)
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78.6%;
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                                                                                                                                              Score 66; DB Pred. No. 0.00
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Pred. No.
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0.005;
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Title:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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102
1 QQQEAKICHQIEYY
PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                   QQQEAKICHQIEYYFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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83

Result

Result No.	Score	% Query Match	Length	BB	ID	ription
1	87	85.3	404	ᆈ	803849	ribonucleoprotein
N	87	85.3	408	μ	A31888	ribonucleoprotein
ω	87		415	ч	JC1494	ribonucleoprotein
4	66	•	427	<u>, .</u>	S33817	ribonucleoprotein
ហ	66	64.7	428	بر	S33818	ribonucleoprotein
თ	57	•	390	N	A53773	La/SS-B homolog D-
7	57		390	N	A53781	ribonucleoprotein
8	52	51.0	391	N	H89777	×
9	50		166	N	T32701	
10	48	٠	529	N	T00677	
11	47		396	N	T30953	
12		•	298	N	T38937	prote
13	46	45.1	298	N	T43542	-binding prot
14	46	45.1	642	ผ	H83743	ABC transporter (p
15	45		352	N	AE2408	hypothetical prote
16		•	506	N	T14907	trans-cinnamate 4-
17	45	٠	568	N	C82379	response regulator
18		•	788	N	A71076	hypothetical prote
19	43.5	42.6	1037	N	E65022	181
20		42.6	1037	N	D91045	'n
21			1037	ผ	G85889	ò
22	43		658	N	D96656	
23	43		658	N	948	- (1
24	43		926	N	S58936 .	
25	43		1131	N	T15617	hypothetical prote
26	42	41.2	242	N	A42478	glutamine transpor
27	42		401	N	AC2207	L-cysteine/cystine
28	42		416	N	S60034	keratin Hal, type
29	42		424	N	T46197	hypothetical prote

45	44	43	42	41	40	39	38	37	36	35	34 4	33	32	31	30
41	41	41	41	41	41	41	41	41	41	41	41.5	42	42	42	42
40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.7	41.2	41.2	41.2	41.2
1220	1220	845	704	506	469	319	251	175	172	51	1428	515	506	505	449
N	ب	N	N	N	N	N	N	N	N	N	N	N	N	N	N
T42573	DJBEC3	T34064	AE2107	F85016	C70357	AF0228	B40969	S23687	F75491	G81188	T13926	T43152	T41623	B90181	G84091
DNA-directed DNA p	DNA-directed DNA p		Ħ	probable King zinc	hypothetical proce	probable transposa	folate-binding pro	erythrocyte membra	conserved hypothet	hypothetical proce	probable procein p	hypothetical proce	probable protein k	Na+/H+ antiporter	hypothetical prote

ALIGNMENTS

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RT clone:P0499C11.";

RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AP001080; BAA90356.1; -.

DR Gramene; Q9LJO2; -.

DR InterPro; IPR006607; DUF DM15.

DR InterPro; IPR006630; Lupus_La_dom.

DR SMART; SM00684; DM15; 3.

DR SMART; SM00715; LA; 1.

DR SMART; SM00715; LA; 1.

SQ SEQUENCE 928 AA; 103745 MW; 53FC46E24A446EB4 CRC64;

SQ SEQUENCE 928 AA; 103745 MW; 53FC46E24A446EB4 CRC64;

Query Match

Best Local Smilarity 61.5%; Pred. No. 57;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps O;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps O;

Search completed: September 10, 2004, 18:00:02

Job time: 44.229 secs
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RESULT
Q9KKL7
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Best Local S
Matches 7
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InterPro; IPR002048; EF-hand.
InterPro; IPR000651; RasGERN.
InterPro; IPR001895; RasGER_CDC25.
InterPro; IPR001895; RasGER_CDC25.
InterPro; IPR0018937; Ras_GEF.
Pfam; PF00130; DAG_PE_bind; 1.
Pfam; PF00036; efhand; 2.
Pfam; PF00036; efhand; 2.
Pfam; PF00010; Caparation of the compart of
                                                                                                                                                                                                                                                                                    PROSITE;
Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U78171; AAD12742.1; -.
EMBL; AF081193; AAC79697.1; -.
HSSP; P28867; 1PTO.
MGD; MGI:1333849; Rasgrp2.
GO; GO:0005509; F:calclum ion binding; IEA.
GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawasaki H., Springett G.M., Toki S., Canales J.J., Harlan P.,
Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N., Ashbacher A.,
Matsuda M., Housman D.B., Graybiel A.M.;
"A Rap guanine nucleotide exchange factor enriched highly in the basal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9QUG9;
01-MAY-2000
                                                                                                                                                                                                                                                                SEQUENCE
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Chen E.J., Bany I.A., Mochizuki N., Ad
Housman D.E., Graybiel A.M.;
"A Novel Rap Guanine Nucleotide Exchar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Kawasaki H., Housm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ganglia.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99007305; PubMed=9789079;
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                      14
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                                                                                                                              N
                                                                                                                                                                                                Similarity
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PS50212; RASGEF_NTER; 1.
Calcium-bindin
                                                                                                                            ALQAKICHQIQYYFGQF 18
                                                                                      SLQVKTCHLVRYWVSAF
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(FEB-1999)
                                                                                                                                                                                                                                                                809
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                    -binding
                                                                                                                                                                                                                                                                69294 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.A.
                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Graybiel A.M.;
e EMBL/GenBank/DDBJ
                                                                                                                                                                       4.
                                                                                                                                                                                              Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                             DC717794CE12C2D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95:13278-13283 (1998)
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                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., Canales J.J., Blumenstiel Ashbacher A., Matsuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      guanine nucleotide exchange
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                                                                                                                                                                         6
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; Murinae; Mus
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RESULT 15
Q9LJ02
ID 09LJ0
AC Q9LJ0
DT 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DE Simil
OS OTYZZZ
OC ELETH
OC STRAL
RA SASAI
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RA SASAI
RA SASAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IR EMBL; AB004434; AAF95979.

JR PIR; C82379; C82379.

JR HSSP; P52934; 1QMP.

JR TIGR; VCA1086; -.

DR GO; GO:0003874; F:Catalytic activity; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR GO; GO:000156; F:two-component response regulator activity; IEA.

DR GO; GO:000166; P:sensory perception; IEA.

DR GO; GO:000160; P:sensory perception; IEA.

DR GO; GO:000160; P:two-component signal transduction system (p. ...

ThterPro; IPR001793; PegC-like

DR InterPro; IPR001793; Response reg.

DR InterPro; IPR001798; Response reg.

DR InterPro; IPR00172; response reg; 1.
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 6
                                                                                                                                                 Q9LJ02 PRELIMINARY;
Q9LJ02;
01-OCT-2000 (TrEMBLrel. 15, Cr
01-OCT-2000 (TrEMBLrel. 25, La
01-OCT-2003 (TrEMBLrel. 25, La
Similar to KJAA0731 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-El Tor N16961 / Serotype 01;

MEDLINE-20406833; PubMed-10953301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Vanathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KKL7;
Q9KKL7;
01'-OCT-2000
01-OCT-2000
01-OCT-2003
                                                                                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T
"Oryza sativa nipponba
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50110; RESPONSE_REGULATORY; 1.

Phosphorylation; Sensory transduction; Complete SEQUENCE 568 AA; 64331 MW; 87A02A350D986F51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00072; response_reg; 1.
Probom; PD000039; Response_reg; 1.
SMART; SM00331; PP2C_SIG; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                             STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: THE N-TERMINAL REGULATORY COMPONENTS OF SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
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                                                SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes cholerae.":
                                                                                                                                                                                                                                                                                                          156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE004434; AAF96979.1;
                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                    LOAKICHQIQYYFG
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nilarity 42.9%;
Conservative
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   nipponbare(GA3) genomic
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15,
25,
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                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 35; 5; Mismatches
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No.
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    DNA,
                                                                                                         Embryophyta; Trach
a; Poales; Poaceae;
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      chromosome
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Best Local
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SEQUENCE FROM N.A.
STRAIN-Reymolds and Newman;
STRAIN-Reymolds and Newman;
MEDLINE-97388587; PubMed-9245821;
MEDLINE-97388587; PubMed-9245821;
Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.
Sau S., Bhasin N., Wann term, Lee J.C., Foster T.J., Lee C.Y.
The Staphylococcus aureus allelic genetic loci for serotype
"The Staphylococcus aureus allelic genetic genes flanked by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sau S., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; GO; GO:0009103; P:11popolysaccharide biosynthesis; IEA. GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA. InterPro; IPR003331; Epimerase_2. Pfam; PF02350; Epimerase_2; 1. TIGR02336; WecB; 1. TIGRO2356; WecB; 1. SEQUENCE 391 AA; 44247 MW; 1E8D9FAA9BC76F0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=Becker;
                                                                                                           STRAIN-Reynolds and Newman;
MEDLINE-98101481; PubMed-9440531;
Kiser K.B., Lee J.C.;
"Staphylococcus aureus cap50 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 178:2118-2126(1996).
                                                                   mutations affecting enterobacterial common-antigen biosynthesis in Escherichia coli.";

J. Bacteriol. 180:403-406(1998).
                                                                                                                                                                                                                                                                             Staphylococcus aureus Bacteria; Firmicutes; NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                        01-MAY-1997
01-JUN-2003
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MEDLINE=98125727; PubMed=9466251;
Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S.,
"Identification of a gene essential for O-acetylation of t
Staphylococcus aureus type 5 capsular polysaccharide.";
                                STRAIN=Reynolds and Newman;
MEDLINE=98125727; PubMed=94
                                                                                                                                                          SEQUENCE FROM N.A.
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Last annotation update)
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Pred. No.
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Q99X57;
01-JUN-2001
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

BMBL; U81973; AAC46099:1; -.

HMSP; P27828; 1F6D.

GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;
GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
InterPro; IPR003331; Epimerase_2.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Capsular polysaccharide synthesis enzyme Cap5P.
CAPP OR SAV0164 OR SA0159.
                                                                                                                                                                                            Complete
SEQUENCE
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GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;
GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
InterPro; IPR003331; Epimerase_2.
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SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shibi
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02350; Epimerase_2; 1
TIGRFAMs; TIGR00236; wecB; 1.
SEQUENCE 391 AA; 44328 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillales; Staphylococcus.
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STRAIN=Reynolds
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EMBL; AP003358; BAB56326.1;

EMBL; AP003129; BAB41379.1;

PIR; H89777; H89777.
                                                                                                                                                                                                                                            InterPro; IPR003331; Epimera
Pfam; PF02350; Epimerase_2;
TIGRFAMs; TIGR00236; wecB; 1
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391 AA;
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SEQUENCE FROM N.A.

RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y.Y., Li C., Li T., Zhang Y.Y., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., RA Zhang R.Q., Guan J.P., Hong G.F.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

BOR SEQUENCE 863 AA; 96838 MW; BACE2362CCF2F296 CRC64;
                                                                                                                                                                                        Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Locate S., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny B.A.C., Shevchenko Y., Bouffard G.G.,

A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.S.,

A A Rodriguez A.C., Stalska U., Smailus D.E., Schnerch A., Schein J.S.,
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
SEQUENCE FROM N.A
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OSJNBB0046P18.10
                                                                                      Jones S.J., Marra M.A.;
"Generation and initial analysis
and mouse cDNA sequences.";
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Mammalia; Eutḥeria;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
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Rodentia;
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                                                                   99:16899-16903 (2002)
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a; Poales; Poaceae;
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Best Local
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                                                P72382
P72382;
01-FEB-1997
01-FEB-1997
01-JUN-2003
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01-OCT-2002
01-JUN-2003
      Cap8P.
CAP8P.
Staphylococcus aureus
Bacteria; Firmicutes;
                                                                                                                                                                                                                                  Complete
SEQUENCE
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EMBL; AP004822; BAB94004.I; -.

GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;

GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.

GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                            Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-acquired MRSA."; Lancet 359:1819-1827(2002).
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., (
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L
                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain MW2)
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capsular polysaccharide CAP8P OR MW0139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000651; RasGEFN.
InterPro; IPR008937; Ras GEF.
SMART; SM00229; RasGEFN; 1.
PROSITE; PS50212; RASGEF NTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC051474; AAH51474.1; -. GO; GO:0005085; F:guanyl-nucleotide GO; GO:0007264; P:small GTPase media
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Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBa
                                                                                                                                                                                                                                                      Pfam; PF02350; Epimerase 2; 1.
TIGRFAMs; TIGR00236; wecB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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141 AA; 16186 MW;
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                                                                                                                                                 RICEAIEYYFG
                                                                                                                                                                  KICHQIQYYFG
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                                                                                                                                                                                                                                                                         IPR003331; Epimerase_2.
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                                                 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                           PRELIMINARY;
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        Bacillales;
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24,
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Last
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Pred.
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Pred. No. 16;
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242C314B00AD9191
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mediated signal transduction; :
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                                                 sequence update) annotation updat
        Staphylococcus
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RESULT 5

Q7ZTIO

ID Q7ZTIO PRELIMINARY; PRT; 401 AA.

AC Q7ZTIO;

O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-JUN-2003 (TrEMBLrel. 26, Last sequence update)

DC cyprinidae; Danio.

OC Eukaryott, Metazao; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RR SEQUENCE FROM N.A.

RI SUBBEDGAY;

RN SUBBEDGAY;

RN SUBBEDGAY;

RN SUBBEDGAY;

RN SUBBEDGAY;

RN SUBBEDGAY;

InterPro; IPR006534; Cinucleus; IEA.

DR GO; GO:0003723; F:RNA binding; IEA.

DR GO; GO:0003723; F:RNA binding; IEA.

DR InterPro; IPR006530; Lupus_La.

DR InterPro; IPR006530; Lupus_La.

DR InterPro; IPR006530; Lupus_La.

DR FRINTS; PR00303; LUPUSLA.

DR SMART; SM00715; LA; 1.

DR PROSITE; PS50103; RRM, RNP_1; 1.

DR PROSITE; PS500030; RRM, RNP_1; 1.

DR PROSITE; PS500030; RRM, RNP_1; 1.

DR PROSITE; PS500030; RRM, RNP_1; 1.
              ACCOMPANA TO THE REPORT OF THE RESERVE TO THE RESERVE 
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Q9UL65
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Best Local S
Matches 8
"Trifunovic J., Clark M., Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
"The germinal center kinase gene and a novel CDC25-like gene located in the vicinity of the PYGM gene on 11q13.";
Hum. Genet. 100:611-619(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, 0
01-MAY-2000 (TrEMBLrel. 13, 1
01-OCT-2003 (TrEMBLrel. 25, 1
Guanine exchange factor MCG7
                                                                                                                                                                                                                                                                                                                              MEDLINE=20493616; PubMed=10918068; Clyde-Smith J., Silins G., Gartside M., Grimmond S., Etheridge Clyde-Smith J., Silins G., Gartside M., Grimmond S., Etheridge Rapolloni A., Hayward N., Hancock J.F.; Apolloni A., Hayward N., Hancock J.F.; Characterization of RasGRP2, a Plasma Membrane-targeted, Dual Specificity Ras/Rap Exchange Factor."; J. Biol. Chem. 275:32260-32267(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL65 PRE
Q9UL65; 000538;
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57.1%;
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form 1 (F25B3.3 kinase like
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RESULT 7 Q7XQ50-ID ,Q7XC

,Q7XQ50

PRELIMINARY;

PRT;

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Best I
                                                 Matches
                                                                                              pfam; pF00036; efhānd; 2.
pfam; pF000617; RasGEF; 1.
SMART; SM00109; C1; 1.
SMART; SM00109; C1; 1.
SMART; SM00229; RasGEFN; 1.
SMART; SM00229; RasGEFN; 1.
PROSITE; pS000479; DAG PE BIND DOM_1; 1.
PROSITE; pS00018; EF HAND; 2.
PROSITE; pS00018; EF HAND; 2.
PROSITE; pS00019; RASGEF_CAT; 1.
PROSITE; PS50012; RASGEF_NTER; 1.
PROSITE; PS501212; RASGEF_NTER; 1.
SEQUENCE 671 AA; 75547 MW; 67B7BDZB4F4AED4D CRC
                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99007305; PubMed-9789079;
Kawasaki H., Springett G.M., Toki S., Canales J.J., H.
Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N.,
Matsuda M., Housman D.E., Graybiel A.M.;
"A Rap quanine nucleotide exchange factor enriched hic
                                                                                                                                                                                                                                                                                                                          HSSP; P28867; 1PTQ.

Genew; HGNC:9879; RASGRP2.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0019992; F:diacylglycerol binding; IEA.

GO; GO:0005085; F:guanyl-nucleotide exchange

GO; GO:0005289; F:lipid binding; TAS.

GO; GO:0007165; P:signal transduction; TAS.

GO; GO:0007264; P:small GTPase mediated signa
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y12336; CAA73005.1; -.
EMBL; U78170; AAD12741.1; -.
EMBL; AF081194; AAC79698.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterisation of a Novel Nucleotide Exchargumentted (JAN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 63-671 FROM N.A. Silins G.U., Grimmond S., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ganglia.";
Submitted (JUL-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Housman D.E., Graybie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawasaki H., Housman D.E., G
Submitted (FEB-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 63-671 FROM N.A. Kawasaki H., Housman D.E., G
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                                                                                                                                                                                                                                                 InterPro; IPR000651; RasGERN.
InterPro; IPR001895; RasGEF CDC25.
InterPro; IPR009397; Ras GEF
Pfam; PF00130; DAG_PR-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 63-671 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawasaki H.
                                                                                                                                                                                                                                                                                         InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR002048; EF-hand.
InterPro; IPR000651; RasGEFN.
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                                                             Local
                                                                        Match
132
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AF043723; AAF07220.1; -.
                       N
                                              7; Conserv
SLOVKTCHLVRYWISAF
                        ALOAKICHQIQYYFGQF
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E., Graybiel A.M.;
pp Guanine N...
                                                 Conservative
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                                                             48.0%;
41.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graybiel A.M.;
e EMBL/GenBank/DDBJ
 148
                        18
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                                                 4.
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Pred.
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                                                  Mismatches
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/GenBank/DDBJ databases
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                                                                          DB
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A., Matsuda
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                                                                          Length 671;
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RESULT
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AC Q8
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DT 01
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Best Local S
Matches 14
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Best Local S
Matches 14
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GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR005634; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
            Q8QHI5
Q8QHI5;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8BTU4;
Q8BTU4;
01-MAR-2003
                                                                                                                                                                                                    PRINTS; PR00302; LUPUSLA.

SMART; SM00305; LA; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM RNP_1; 1.

SEQUENCE 415 AA; 47657 MW; 1
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SMART; SM00715; LA; 1.
SEQUENCE 381 AA; 43891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002344; Lupus_La.
InterPro; IPR00630; Lupus_La_dom.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR006030; RNA_rec_mot.
pfam; pF05383; La; 1.
pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sjogren syndrome antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRALN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005634; C:nucleus;
                                                                                                                                                                                                                                                                                                                                                   EMBL; AK088677; BAC40498.1; -.
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ALEAKICHQIEYYFGDF 28
                                                                                                              ALQAKICHQIQYYFGQF 18
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(TrEMBLrel. 21, 1
(TrEMBLrel. 25, 1
d region binding-
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                                    (TrEMBLrel.
                                                         PRELIMINARY;
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Rodentia;
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            21, Created)
21, Last sequence update)
25, Last annotation updat
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Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                                     Score 83;
Pred. No.
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                                                          PRT;
                                                                                                                                                                                                      A7545C7686AC8363 CRC64;
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9.6e-06;
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8.8e-06;
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              update)
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RESULT 4
Q7ZTK2
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Best Local S
Matches 10
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L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMBL/
EMBL; AF467897; AAL76269.1; -.

GO; GO:0005634; C:nucleus; IEA.
GO; GO:0007723; F:RNA binding; II
                                                                                                                                                                    Pfam; PRO0076; rrm; 1.
PRINTS; PRO0302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 2.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7ZTK2
Q7ZTK2;
Q1-JUN-2003 (
Q1-JUN-2003 (
Q1-OCT-2003 (
                                                                                                                                                                                                                                                                               Klein S., Strausberg R.;
Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046654; AAH46654.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus_La.
InterPro; IPR00630; Lupus_La.
InterPro; IPR00630; Lupus_Com.
InterPro; IPR00630; RNA_rec_mot.
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01-JUN-2003 (TrEMBLrel. 25, Last sequer
01-OCT-2003 (TrEMBLrel. 25, Last annote
Similar to lupus LA protein homolog B.
Stenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UBP.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ve:
Amphibia; Batrachia; Anura; Mesobatrachia;
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PROSITE; PS00030; RRM_RNP_1;
SEQUENCE 206 AA; 23992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
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InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
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                                                                         Similarity
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                                                     Conservative
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                                                                                                                                                     48996 MW;
                                                                            60.2%;
71.4%;
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                                                                         Score 59;
Pred. No.
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                                                                                                                                                     1E7CD82D8AB9C69A CRC64;
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                                                Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                               Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                      SPTREMBL 25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate
14: sp_virus:*
15: sp_bacteriap::
16: sp_bacteriap:
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98
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137.751 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                    sp_organelle:*
sp_phage:*
sp_plant:*
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sp_invertebrate:*
sp_mammal:*
SUMMARIES
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TO TO CAMOUA	0 028 10 001.T02	.9 568 16 Q9KKL7	11 Q9QUG9	391 16 Q99X57	11 46 46.9 391 2 P95709 P9	391 2 P72382 I	381 16 Q8NYN8	141 11 Q80WC0	863 10 Q7XQ50	48.0 671 4 Q9UL65 Q	401 13 Q7ZTIO	60.2 427 13 Q7ZTK2	63.3 206 13 Q8QHI5	84.7 415 11 Q8BTU4	84.7 381 11 Q9CYB9	Result Query No. Score Match Length DB ID
Contracting Contraction of	•	Q9kkl7 vibrio chol	Q9qug9 mus musculu	099x57 staphylococ	P95709 staphylococ	P72382 staphylococ	Q8nyn8 staphylococ	Q80wc0 mus musculu	Q7xq50 oryza sativ	Q9ul65 homo sapien	Q7zti0 brachydanio	Q7ztk2 xenopus lae	Q8qhi5 gallus gall		Q9cyb9 mus musculu	Description

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41.8	41.8	41.8	41.8			٠	41.8			41.8	41.8		42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9			43.9	44.9
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ALIGNMENTS

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SEQUENCE FROM N.A. STRAIN=C57BL/6J; TMEDLINE=2108566; Kawai J., Shinagaw Alrakawa T., Hara Alaivawa K., Izawa W Saito T., Okazaki Kadota K., Matsuda Fleischmann W., Ga Kuehl P., Lewis Sakai K., Okido T. Blake J., Boffelli Brownstein M.J., Ellyons P., Marchior Nordone P., Ring E Sasaki H., Toto-ok Wynshaw-Boris A., Hayashizaki Y.; WGD; MGI:98423; Se	UT 1 OPCYB9 PRELIMIN OPCYB9; O1-JUN-2001 (TrEMBLz O1-JUN-2001 (TrEMBLz O1-OCT-2003 (TREMBLz O1-OCT-2003 (TREMBLz Sjogren syndrome ant SSB. Mus musculus (Mouse) Eukaryota; Metazoa; Memmalia; Eutheria; NCBI_TaxID=10090;
SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851; KAWAI J., Shinagawa A., Shibata K., Yoshino M., Arakawa T., Hara A., Fukunishi Y., Konno H., Ada Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kon Saito T., Okazaki Y., Gojobori T., Bono H., Kas Kadota K., Matsuda H.A., Ashburner M., Batalov Fleischmann W., Gaasterland T., Gissi C., King Kushl P., Lewis S., Matsuv Y., Nikaido I., Peso Schriml L.M., Staubli F., Suzuki R., Tomita M., Sakai K., Okido T., Furuno M., Aono H., Baldare Blake J., Beffelli D., Bojunga N., Carninci P., Brownstein M.J., Bult C., Fletcher C., Fujita M. Gustincich S., Hill D., Hofmann M., Hume D.A., Lyons P., Marchionni L., Mashima J., Mazzarelli Nordone P., King B., Ringwald M., Rodriguez I., Sasaki H., Sato K., Schoenbach C., Seya T., Shi Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wah Hayashizaki Y.; Functional annotation of a full-length mouse c Nature 409:685-690(2001) EMBL; AK017822; BaB30957.1;	T 1 Q9CYB9 PRELIMINARY; Q9CYB9; Q1-JUN-2001 (TrEMBLrel. 17, L 01-JUN-2001 (TrEMBLrel. 25, L 01-JCT-2003 (TrEMBLrel. 25, L 01-GT-2003 (TrEMBLrel. 25, L 01-GT-01000 (TrEMBLrel. 17, C 01-GT-01000 (TrEMBLrel. 17, L 01-GT-01
SUE=Embryo; bMed=11217851; A., Shibata K., Yoshino M., Fukunishi Y., Konno H., K., Mishi K., Kiyosawa H., K., Gojobori T., Bono H., K., Gojobori T., Bono H., K., Gojobori T., Bono H., Batalorterland T., Gissi C., Kinematsuo Y., Nikaido I., Peruno M., Aono H., Balda Puruno M., Mono H., Balda Puruno M., Aono H., Balda Puruno M., Aono H., Balda Puruno M., Aono H., Walta M., Rodriguez I., Mashima J., Mazzarel R., Mashima J., Mazzarel R., Mashima J., Waitz C., I., Schoenbach C., Seya T., Si K., Wang K.H., Weitz C., I., Shida K., Hasegawa Y., Kaishida K., Hasega	מו מו או
M., Itc Adachi Kondo S Kasukau OV S., OV S., esole (esole (esole (m., Wan M., Wan M., de P., de P., de I., Sal II., Sal II., Sal II., Sal Shibatt Shibatt Shibatt awaji I	a; E
bh M., Ishii Y., [J., Fukuda S., 3, Yamanaka I., va T., Saito R., CCasavant T., Kochiwa H., yackenbush J., guackenbush J., gua	Euteleostomi; Murinae; Mus.

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Query Match
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Matches 7
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                            InterPro; IPR003612; AAI.
InterPro; IPR001954; Glia_glutenin.
InterPro; IPR001954; Glia_glutenin.
InterPro; IPR000480; Glutelin.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00218; GLIADGLUTEN.
PRINTS; PR00211; GLUTELIN.
SMART; SM00499; AAI; 1.
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01-AUG-1988 (Rel. 08, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Zein-beta precursor (Zein 2) (16 kDa) (Zein ZCl).
Zean-seta (Zein 2) (16 kDa) (Zein ZCl).
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STRAIN-cv. W64A; TISSUE-Endosperm;
STRAIN-cv. W64A; TISSUE-Endosperm;
MEDLINE-91057131; PubMed-2243787;
Reina M., Guillen P., Ponte I., Boronat A., Palau J.;
Reina M., Guillen P., Ponte I., Boronat A., Palau J.;
"DNA sequence of the gene encoding the Zc1 protein from Zea mays W64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=87248094; PubMed=3596247;

MIDLINE=87248094; PubMed=3596247;

Prat S., Perez-Crau L., Pujgdomenech P.;

"Multiple variability in the sequence of a family of maize endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16460; AAA33523.1; -. EMBL; X53515; CAA37595.1; -. PIR; B29017; B29017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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01-AUG-1988
                                                                                                                                                                        Seed storage protein; Repeat; Multigene family; Signal
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39.8%; Score 39; DB 1; Length 183; 63.6%; Pred. No. 15; tive 2; Mismatches 2; Indels
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Search completed: September 10, 2004, 17:53:03 Job time : 8.24022 secs

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P39480; OSKTRO;
01-APR-1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Toxin coregulated pilus biosynthesis protein
                                     SEQUENCE FROM N.A.

STRAIN-EI TOR N16561 / Serotype 01;

MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.

Fraser C.M.;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Classical Inaba Z17561 / Serotype O:
STRAIN=Classical Inaba Z17561 / Serotype O:
MEDLINE=93211537; PubMed=8097178;
Ogierman M.A., Zabihi S., Mourtzios L., Mai
"Genetic organization and sequence of the property of the top gene cluster of Vibrio cholerae.";
Gene 126:51-60(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
VCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diosynthesis protein tcpT).
TCPT OR VC0835.
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PRODOM; PD000018; WD40; 2.
SMART; SM00320; WD40; 2.
PROSITE; PS00678; WD REPEATS 1; 2.
PROSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50294; WD_REPEATS_REGION;
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Pfam; PF00400; WD40;
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AY054181; AAL06842.1; ALT_INIT.
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RESULT 14
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ID - CY2 RHOVA
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Best Local
                                                                                                         PIR; A00074; CCRD2.

HSSP; P00083; ICRY.

InterPro; IPR003088; Cyt_CI.

InterPro; IPR002327; Cyt_CIAB.

InterPro; IPR002345; Cyt_Cheme_BS.

Pfam; P700034; CytCChrome_C; 1.

PRINTS; PR00604; CYTCHRMEGIAB.

ProDom; PD000375; Cyt_CIAB; 1.

PROSITE; P800190; CYTGCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ambler R.P., Meyer T.E., Kamen M.D.;

Primary structure determination of two cytochromes c2: close
similarity to functionally unrelated mitochondrial cytochrome C.";

Proc. Natl. Acad. Sci. U.S. A. 73:472-475 (1976)

-I- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,

PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR
TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION

PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHA

AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodomicrobium vannielii.
Batteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Hyphomicrobiaceae, Rhodomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO01482; GSPII_E.
Pfam; PPO0437; GSPII_E; 1.
ProDom; PD000739; GSPII_E; 1.
PROSITE; PS00662; T2SP_E; 1.
Transport; ATP-binding; Complete proteome.
Transport; ATP-binding; ATP (POTENTI)
NP_BIND 236 243 ATP (POTENTI)
CONFLICT 137 137 A > S (IN RE
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EMBL; AE004168; AAF93998.1; -.
PIR; F82275; F82275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: INVOLVED IN THE TRANSLOCATION OF THE TCPA PILIN.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE PULE/OUTE/EXEE/XPSE/XCPR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 17100;
MEDLINE=76102814; PubMed=174109;
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01, Last sequence 42, Last annotations
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; ED3FD8FFD579F918 CRC64;
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Pred. No. 35;
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RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA James K., Jones H., Leather S., McDonald S., McLean J., RA James K., Jones M., Leather S., McDonald S., McLean J., RA James K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Qliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Goliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Whitehead S., RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Ra Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., RA Gabel C., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Ra Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";

RI Nature 415:871-880(2002).
                                                                                                                                                 GenebB_SPombe; SPAC1B3.04c; -.
InterPro; IPR000795; EF_GTBbind.
InterPro; IPR000640; EFG_C:
InterPro; IPR009022; EFG_III_V.
InterPro; IPR004161; EFTU_D2.
InterPro; IPR006297; LepA.
InterPro; IPR005225; Small_GTP.
InterPro; IPR005225; Small_GTP.
InterPro; IPR009000; Translat_factor.
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15-JUL-1998
28-FEB-2003
TIGREPAMS; TIGRO1393; lepA; 1.
TIGREPAMS; TIGRO231; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
Hypothetical protein; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                         Pfam; PF00679; EFG_C; 1.
Pfam; PF000679; GTP_EFTU 1.
Pfam; PF03144; GTP_EFTU D2; 1.
PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                EMBL; Z98598;
PIR; T38022; T
                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                  T38022.
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Yamada K., Lim J., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wa J., Carninci P.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Kakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banh J., Bonno F., Bowser L., Brooks S.Y., Carninci P.,

A Hayashizaki Y., Johnson-Hopson C., Hsuan V.M., Iida K., Karnes M.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
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Best Local
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Q39130, Q34Q7; Q9LUR9;

15-JUL-1998 (Rel. 36, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

15-MAR-2004 (Rel. 43, Last annotation update)

19P1/PP2A phosphatases pleiotropic regulator PRL2.

PRL2 OR AT3G16650 OR MG16.11.

Arabidopsis thaliana (Mouse-ear cress).

Spermatophyta; Wiridiplantae; Streptophyta; Embryophyta

Spermatophyta; Magnollophyta; eudicotyledons; Core

surosids II; Brassicales; Brassicaceae; Arabidopsis

NUBI TaxID=3702;
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NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE-98438452; PubMed-9765207;
MEDLINE-98438452; PubMed-9765207;
Nemeth K., Salchert K., Putnoky P., Bhalerao R., Koncz-Kalman Z.,
Stankovic-Stangeland B., Bako L., Mathur J., Okresz L., Stabel S.
Geigenberger P., Stitt M., Redei G.P., Schell J., Koncz C.;
"Pleiotropic control of glucose and hormone responses by PRL1, a
nuclear WD protein, in Arabidopsis.";
Genes Dev. 12:3059-3073(1998).
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clones.";
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Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC
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                                                                                                                       genome.";
Science 302:842-846(2003).
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                GAUTION:
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                                                  FUNCTION: Pleiotropic regulator of PE
SIMILARITY: Contains 7 WD repeats
SIMILARITY: Belongs to the WD-repeat
CAUTION: Ref. 2 sequence differs from
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K., Ansari Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98114590; PubMed=9398535;
Mikura T., Hirata R., Weil S.C.;
"A novel interferon-inducible gene expressed during myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFTS_HUMAN
Q13325;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
           Repeat; TPR
REPEAT
                             Pfam; PF00515; TPR; 5
SMART; SM00028; TPR; 5
                                                                                       EMBL; U34605; AAA84934.1; -.
EMBL; BC025786; AAH25786.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentiation."
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Mammalia; Eutheria; Primates;
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                                                InterPro; IPR008940; Prenyl_trans
InterPro; IPR001440; TPR.
                                                                   PIR; G02058; G02058.
Genew; HGNC:13328; 1
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30-MAY-2000 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Interferon-induced protein with tetratricopeptide repeats 5 (IFIT-5)
(Retinoic acid- and interferon-inducible 58 kDa protein).
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repeat; Interferon induction.
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94 127 TPR 2.
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SEQUENCE
                                                                                  Pfam; PF00136; DNA_DOL_B; 1.—
Pfam; PF03104; DNA_DOL_B; 1.

PRINTS; PR0106; DNAPOLES
SMART; SM00486; POLBC; 1.

PROSITE; PS00116; DNA_POLYMERASE B; 1.

Transferase; DNA_directed DNA_POTymerase; DNA_replication;
DNA_binding; Nuclear protein.

SEQUENCE 1220 AA; 135956 MW; 858C14DCCC71A65B CRC64;
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01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                  EMBL; M86664; AAB02465.1; -. PIR; D36798; DJBEC3.
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                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92295566; PubMed=1318606; Telford E.A.R., Watson M.S., McBride K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                            InterPro; IPR006172; DNA pol B.
InterPro; IPR006134; DNA pol B dom.
InterPro; IPR006133; DNA pol B exo.
                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pardigon N., Strauss J.H.;

"Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";

J. Virol. 70:1173-1181(1996).

-I- FUNCTION: May be involved in transcription termination by RNA
polymerase III. Binds RNA and DNA. Binds to the 3' end of the
minus strand of Sindbis virus RNA. This may be significant for
Sindbis virus RNA replication.

-I- SUBCELIULAR LOCATION: Nuclear. Primarily nuclear, but significan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X68817; CAA487
PIR; S33818; S33818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Nematocera; Culi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q26457;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50102; RRM; 1. PROSITE; PS00030; RRM_RNP
                                                                                                                                                                                                 entities requires a license agreemen or send an email to license@isb-sib.
                                                                                                                                                                                                                                                 modified and this statement
                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=96135233; PubMed=8551578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LA AEDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006630;
InterPro; IPR000504;
                                                                    InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro; IPR002344;
                         Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                 EMBL; S80954; AAB35931.1; -
                                                                                                                                                                                                                                                                                                                                                                                                amounts are present in the cytoplasm.
SIMILARITY: Contains 1 RNA recognition motif
SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                        European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X68817; CAA48715.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
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9; Conser
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an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KICEQIEYYFG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KICHQIQYYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0030; RRM RNP 1; 1.

Nuclear protein; Phosphorylation.

111 203 RNA-BINDING (RRM).

196 212 NUCLEAR LOCALIZATION SIGNAL

316 332 NUCLEAR LOCALIZATION SIGNAL

316 332 NUCLEAR ADDITION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Lupus_La_dom.
RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
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81.8%;
                                                                                                                                                                                                                                               is not
                                                                                                                                                                                                                             agreement (See
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Pred. No. 0.061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                 removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
                                                                                                                                                                                                                                                                      There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (La
                                                                                                                                                                                                                          http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                               Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoantigen homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 428,
                                                                                                                                                                                                                                                                                                                                                                                                                            (RRM)
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                                                                                                                                                                                                                                                                                                                                                                                                                               domain
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                                                                                                                                                                                                                                                                                                                           EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          significant
                                                                                                                                                                                                                                                                                                                                                  a collaboration
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Query Match Best Local S Matches

8; Conserv

Conservative

43.9%; 47.1%;

Score 43; Pred. No.

DB

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Length 602;

Mismatches

6

Indels

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Gaps

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EXSAULT

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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishika "Genome sequence of the endocellular bacterial symbiont Buchnera sp. APS.";
Nature 407.81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50102; RRM; 1.

PROSITE; PS501030; RRM; RNP 1; FALSE NEG.
RNA-binding; Nuclear Protein; DNA-binding.
RNA-binding; Nuclear Protein; DNA-binding.
RNA-BINDING (RRM).
DOMAIN
141
228
RNA-BINDING (RRM).
SEQUENCE 383 AA; 44430 MW; 4E5CCBF21C40F452 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001
16-OCT-2001
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SMART; SM00360;
                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             symbiotic bacterium).
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
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                                   Ą
                                                                               Hydrolase; Nuclease;
                                                                                                  TIGREAMS; TIGRO1447; recD; 1
                                                                                                                                   EMBL; AP001119; BAB13153.1; -
InterPro; IPR003593; AAA ATPase.
InterPro; IPR006344; RecD.
SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=118099;
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     SEQUENCE
                                                         DNA repair;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                              BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: EXHIBITS SEVERAL CATALYTIC ACTIVITIES, INCLUDING ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED ENDOMUCLEASE, ATP-DEPENDENT EXONUCLEASE, ATP-DEPENDENT OF AND DAN-DEPENDENT ATPASE ACTIVITIES. STRAND CLEAVAGE OCCURS 5 TO 3 DURING THE UNWINDING OF DUPLEX STRAND CLEAVAGE OCCURS 5 TO 3 DURING THE UNWINDING OF DUPLEX DNA AT CHI SEQUENCES, WHICH LOCALLY STIMULATE RECOMBINATION (BY SIMILARITY).

(BY SIMILARITY).

CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'-13'- or 3'- to 5'-direction to yield 5'-ATP) in either 5'-13'- or 3'- to 5'-direction to yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphooligonucleotides.
SUBUNIT: Consist of three subunits; recB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
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7; Conserv
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     602
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(Rel. 40,
(Rel. 40,
                                                      Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LA; 1.
RRM; 1.
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                                   e proteome
178
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        69494 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V alpha chain
                                                                                  Exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update)
Last annotation update)
Chart annotation (EC 3.1.11.5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB Pred. No. 6.5; 3; Mismatches
                              ATP
        340FFAE9BB436059
                                   (POTENTIAL)
                                                                                    Endonuclease; Helicase;
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6.5;
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          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   presence of yield 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of aphids
                                                                                       ATP-binding;
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RESULT 5
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Best Local S
Matches 14
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PSS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; 1.
PROSITE; PS00030; RRM RNP_1; 1.
PROSITE; PS00030; RRM RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGG; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP005383; La; 1.
Pfam; PP00576; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAB XENLA
P28049;
01-AUG-1992
01-AUG-1992
15-MAR-2004
                                                                                                                                                                                                                                                                                                                J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L00993; AAA39415.1; -.
EMBL; BC003820; AAH03820.1;
EMBL; Y07951; CAA69249.1; -.
                     This
                                                                                                                                                                                                                                                                                                                                                                TISSUE=Oocyte;
MEDLINE=93287095; PubMed=8510143;
Scherly D., Stutz F., Lin-Marq N., Clarkson S.G.;
"La proteins from Xenopus laevis. cDNA cloning and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are use by non-profit institutions as long as its modified and this statement is not removed. Usage entities requires a license agreement (See http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01.AUG-1992 (Rel. 23, Created)
01.AUG-1992 (Rel. 23, Last sequence update)
15.AMR-2004 (Rel. 43, Last annotation update)
Lupus La protein homolog B (La ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAB1.
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                                                        embryos.

PTM: Phosphorylated (Probable).

PTM: Phosphorylated (Probable).

MISCELLANEOUS: There are two forms of La,
SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.

SIMILARITY: Contains 1 RNA recognition mot
                                                                                                                                                                               MOI. Biol. 231:196-204(1993).

FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).

SUBCELLULAR LOCATION: Nuclear (Probable).

DEWELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly.
                                                                                                                                                                  constant steady state level
SWISS-PROT ent
een the Swiss
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415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus.
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  entry is copyright. It is produced iss Institute of Bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47756 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Phosphorylation.
RNA-BINDING (RRM).
; 2D75197692FDC933 CRC64;
                                                                                                                                                                    ä
                                                                                                                                                                    mature
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4e-07;
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                                                              motif (RRM)
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  through a collaboration d the EMBL outstation -
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                                                                                                       LaB,
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European Bioinformatics Institute. The by non-profit institutions as long

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Best Local S
Matches 10
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01-AUG-1992
15-MAR-2004
                                                                                     LAA XENLA
P28048;
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                         MEDLINE=93287095; PubMed=8510143;
Scherly D., Stutz F., Lin-Marq N.,
"La proteins from Xenopus laevis.
                                                                                                                                                                                                                                                                                                                Endna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50102; RRM; 1.

PROSITE; PS0030; RRM RNP 1; FALSE NEG.

RNA-binding; Nuclear protein; Phosphorylation.

DOMAIN

10 202

RNA-BINDING (RRM).

DOMAIN

315 331

NUCLEAR LOCALIZATION SIGNAL

DOMAIN

RNA-BINDING (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00302; LUPUSL
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bicinformatics Institute. The use by non-profit institutions as some modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                               expression.";
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X68818; CAA48716.1; -.
                                                                                                                                                                                                                                                          Kenopodinae; Kenopus.
                                                                                                                                                                                                                                                                                       Kenopus laevis
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PF00076; rrm; 1
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IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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2 (Rel. 23, Last s
4 (Rel. 43, Last a
rotein homolog A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                       (African
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LUPUSLA.
                                                                                                                                                                                                                                                                   ican clawed frog).
Chordata; Craniata; Vertebrata; Euteleostomi;
; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48995 MW;
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71.4%;
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                                                                                                                                                                                                                                                                                                                                    sequence update)
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Pred.
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                                                                                                                                                                                                                                                                                                                   ribonucleoprotein
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                                                                                                                                                                                      Clarkson S.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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0.012;
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                                                                xenopus.
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Best Local
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01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation of rat cDNA clones coding for detection of species-specific variations. Gene 126:265-268(1993)
                                                                                                                                                                                InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rēc_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                     encities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Rodentia;
                       PROSITE; PS50102; RRM; 1.
PROSITE; PS90030; RRM RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
DOMAIN 111 187 RNA-BINDING (RRM)
                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                      PIR; JC1494;
                                                                                                                                                                                                                                                                                                                           EMBL; X67859; CAA48043.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93246255; PubMed=7916708; Semsei I., Troester H., Bartsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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    SEQUENCE
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SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                                             ; PR00302; LUPUSLA.
SM00715; LA; 1.
SM00360; RRM; 1.
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366
408
  415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 31, Created)
(Rel. 31, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87; DB Pred. No. 1.7e
2; Mismatches
    RNA-BINDING (RRM).
; 033FD9CC1E475F98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonucleoprotein)
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EC153C15F9187FC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwemmle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for the autoantigen SS-B/La:
ions.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Igloi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoantigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
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5S, 7S,
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RESULT 4

ILA MOUSE

ID MOA MOUSE

AC P32067;

DT 01-0CT-19

DT 15-MAR-20

DE Lupus La

CO SSB OR SS

OS Mus muscu

OC Eukaryota

OC Mammalia;

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RN [1]

RP SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1993
01-OCT-1993
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of conserved RNA-binding motifs, a putative ATP binding site and reactivity of recombinant protein with poly(U) and human autoantibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93203630; PubMed=8454877;
Topfer F. Gordon T. McCluskey J.
"Characterization of the mouse aut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lupus La protein
                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSB OR SS-B.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-11 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                     PTM: Phosphorylated (By similarity). SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                            and 7-2 RNAs.
SUBUNIT: Interacts with DDX15
SUBCELLULAR LOCATION: Nuclear
PTM: Phosphorylated (By simila
                                                                                                                                                                                                                     nitted (OCT-1996) to the EMBL/GenBank/DDBJ databases. FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S.
        SWISS-PROT entry is copyright.
een the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
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VB/N; TISSUE=Mammary gland;

-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homolog
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27,
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                          N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (La ribonucleoprotein)
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99:16899-16903 (2002)
     ght. It is produced through Bioinformatics and the EM
                                                                                                                                              (Probable)
                                                                                                                                                                     (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoantigen
              EMBL
                                     a collaboration
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              outstation
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RESULT 2
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RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
PYCC. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LA HUMAN
P05455;
01-NOV-1988
01-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Lupus La protein (Sjogren syndrome type B antigen) (SS-B)
ribonucleoprotein) (La autoantigen).
                                                    Sturgess
Coppel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89053970; PubMed=3192525;
MEDLINE-89053970; PubMed=3192525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89202037; PubMed=2468131;
Chan E.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                  SEQUENCE OF 54-408
MEDLINE=88199081; F
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Placenta, and Skeletal musc MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic structure and amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences for 
Nucleic Acids
                                        "Characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Eukaryota; Metazoa; C
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R.S.;
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            140:3212-3218(1988
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Res. 17:2233-2244(1989)
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Primates;
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Catarrhini;
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EMBL; J04205; AAA51885.1; -
EMBL; BC001289; AAH01289.1;
EMBL; BC020818; AAH20818.1;
PIR; A31888; A31888.
                                                                                                                                             MIM; 109090; -.
GO; GO:0030529; C:ribonucleoprotein complex; TAS.
GO; GO:0003729; F:mRNA binding; TAS.
GO; GO:0000049; F:tRNA binding; TAS.
GO; GO:0000334; P:histone mRNA metabolism; TAS.
GO; GO:0006400; P:tRNA modification; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    often contain antibodies that react with the normal cellul
La protein as if this antigen was foreign.
-!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and 7-2 RNAS.

-!- SUBUNIT: Interacts with DDX15.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
-!- PTM: The N-terminus is blocked.
-!- DISEASE: Sera from patients with systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S Van Venrooij W.J., Pruijn G.J.M., "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, "Butative DEAH-box RNA helicase.", RNA 8:1428-1443(2002).

-!- FUNCTION: La protein plays a role in the transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97207017; PubMed=9054510; Fan H., Sakulich A.L., Goodier J.L., Zhang X., "Phosphorylation of the human La antigen on serecycling of RNA polymerase III transcription (cll 88:707-715(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89251617; PubMed=24
Gottlieb E., Steitz J.A.;
"Function of the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILNE=8516628; PubMed=3856888; Chambers J.C., Keene J.D.; "Isolation and analysis of cDNA c
               SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                  Pfam; PF05383; La; 1. Pfam: PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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MEDLINE=22346609; PubMe
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                                                                PF00076;
                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                          IPR002344; Lupus_La.
IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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igen on serine 366 can regulate
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129.452 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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 P00082 rhodomicrob
P00031 zea mays (m
P40796 drosophila
082wi2 nitrosomona
Q0511 human papil
Q10432 schizosacch
Q24087 drosophila
P24307 autographa
P91926 drosophila
P91926 drosophila
O95782 h adapter-r
Q05685 mus musculu
Q9kvt4 vibrio chol
P51692 homo sapien
Q8teq8 homo sapien
P46735 mus musculu
Q05096 rattus norv
Q43593 homo sapien
Q61602 mus musculu
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P05455 homo sapien
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ALIGNMENTS	GATB_CHLCV	GLGA_RHITR	SRO9_YEAST	CASB_KLEOX	Y863_SYNY3	THIC_FUSNN	CARA_BUCBP	CKR3_MOUSE	FDHE_PSEAE	SDGF_RAT	MTNA_BACSU	MOAR_KLEAE
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C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 27-Oct-2003
C;Accession: D36798
R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A;Description: The DNA sequence of equine herpesvirus-1.
A;Reference number: A36805
A;Accession: D36798
                                                                                                                                                                                                                                                                                                                      A;Gene: 30
C;Superfamily: DNA polymerase
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase
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A;Cross-references: GB:M86664; NID:g330791; PIDN:AAB02465.1; PID:g330822
A;Cross-references: GB:M86664; NID:g330791; PIDN:AAB02465.1; PID:g330822
A;Cross-reference GB:M86664; NID:g330791; PIDN:AB02465.1; PID:g330822
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:g2295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
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Best Local Similarity 60.0%;
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Pred. No. 63;
1; Mismatches
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hypothetical protein jhp0797 - Helicobacter pylori (strain J99)

(;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
C;Accession: H71887
C;Accession: H7187, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: H71887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Sammons, L.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, August 1999 A;Description: The sequence of C. elegans cosmid C44E4. A;Reference number: Z20945 A;Accession: T30953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 45/1; 114/3
A; Note: C44E4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-396 <SAM>
A;Residues: 1-396 <SAM>
A;Cxogs-references: EMBL:AF003140; PIDN:AAB54169.1
A;Experimental source: strain Bristol N2; clone C44E4
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-482 <WEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: G02058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, August 1995
A;Reference number: H00758
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                      A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Species: Homo sapiens (man);Date: 21-Dec-1996 #sequence;Accession: G02058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Cross-references: EMBL:U34605; NID:g1144510; PIDN:AAA84934.1; PID:g1144511;Superfamily: interferon-induced 56K protein
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Best Local (
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Pred. No.
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Pred. No. 21;
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Query Match
Best Local Similarity
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2010

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: D9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
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C;Superfamily: Helicobacter pylori hypothetical
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A;Cross-references: GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD06373.1; PID:g415536
A;Experimental source: strain J99
C;Genetics:
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A;Residues: 1-542 <TOM>
A;Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07917.1; PID:g231400
C;Superfamily: Helicobacter pylori hypothetical protein jhp0797
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997
C;Accession: G64627
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A;Gene: F16M19.21
A;Map position: 1
                                                                                                          A; Molecule type: DNA
A; Residues: 1-658 <STO>
                                                                                                                                                            A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Date: 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F16M19.21 [imported] - Arabi
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                              A; Cross-references:
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                                                                                GB:AE005173; NID:g6598840; PIDN:AAF18695.1; GSPDB:GN00141
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Pred. No.
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42.9%; 31.2%;

Score Pred.

42; DB No. 35;

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Length

Mon

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R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental e A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33818
A;Accession: S33818
A;Accession: S33818
A;Accession: S33817; MUID:93287095; PMID:8510143
A;Residues: 1-428 <SCH>
A;Residues: 1-428 <SCH>
A;Cross references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874
A;Cross references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874
C;Comment: This protein associates with a variety of small RNA molecules, ay act as a transcription termination factor.
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: phosphoprotein; RNA binding
C;Keywords: phosphoprotein; RNA binding
C;Reywords: phosphoprotein; RNA binding
C;Reywords: phosphoprotein; RNA binding
C;Reywords: phosphoprotein; RNA protein repeat homology <RRM>
                                                              C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Apr-2003
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Apr-2003
C;Accession: C92379
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M:L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Ritle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C92379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 10.-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: H89777
C;Accession: H89777
R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; (ma, A., Mizutani-Ui, Y; Kobayashi, N.; Sawano, T; Inoue, R; Kaito, C; Sima, A., Mizutani-Ui, Y; Kobayashi, N.; Hayashi, H; Hiramatsu, K. C; Shiba, T; Hattori, M.; Ogasawara, N.; Hayashi, H; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aurel A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89777
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F;151-158/Region: RNA-binding RNP1 motif
F;228-428/Domain: phosphorylated #status predicted
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A;Experimental source: strain N315
                       A;Status: preliminary A;Molecule type: DNA
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A; Residues: 1-391 <KUR>
A;Residues: 1-568 <HEI>
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Pred. No. 4.3;
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H.; Dragoi, I.; Sellers,
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A;Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; A;Ex;erimental source: serogroup O1; strain N16961; biotype C;Genetics: A;Gene: VCA1086
                                                                                                                      A;Status; Processing A;Anolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-577 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81487.1;
A;Cross-references: GD:AE001437; PIDN:AAK81487.1;
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C; Superfamily: response regulator,
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325, A;Accession: D97337
                                                                                                                                                                                                                                                                                                                               mismatch repair protein MutS-like ATPase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D97337
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A;Residues: 1-602 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
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5; Mismatches
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A;Molecule type: mRNA
A;Residues: 1-19,'E',21-47 <NYM>
A;Residues: 1-19,'E',21-47 <NYM>
A;Residues: 1-19,'E',21-47 <NYM>
A;Sturgess, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, R.J.
J. Immunol. 140, 3212-3218, 1988
A;Title: Characteristics and epitope mapping of a cloned human autoantigen La.
A;Reference number: S11013; MUID:88199081; PMID:2452201
A;Accession: S11013
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R;Nyman, U.; Ringertz, N.R.; Pettersson, I.
Immunol. Lett. 22, 65-72, 1989
A;Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
A;Reference number: A61051; MUID:89379261; PMID:2478379
A;Accession: A61051
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A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;RCOB8-references: EMBL:M20128; NID:g337456; PIDN:AAA36577.1; PID:g337457
A;KOhsaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka, J. Clin. Invest. 85, 1566-1574, 1990
A;Title: Fine epitope mapping the human SS-B/La protein: Identification of A;Reference number: I55553; MUID:90237237; PMID:1692037
A;Accession: I55553
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A; Residues: 279-342 < RE3 >
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A; Residues: 174-224 <RE2>
A; Cross-references: GB:M35263; NID:g338492;
A; Accession: I70206
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
A;Reference number: A22956; MUID:85166283; PMID:3856888
A;Accession: A22956.
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A; Accession: S03848
A; Molecule type: mRl
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                                                                                                                 Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                            ;112-178/Domain: ribonucleoprotein repeat homology;113-118/Region: RNA-binding RNP2 motif;151-158/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Gene: GDB:SSB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Accession: I70205
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:Residues: 45-97,'LK' <CH3>
                                                                                                                                                                                                                                                                                                                                                  Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
Residues: 81-107 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                228-408/Domain: phosphorylated
   11
                                                                                                                                                Similarity
                                                       AALQAKICHQIQYYFGQF 18
   AALEAKICHQIEYYFGDF
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDB:125359; OMIM:109090
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28
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                                                                                                                                             Score 87;
Pred. No.
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                                                                                                                                                3.7e-07;
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RESULT 3

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RESULT 5
S33818
ribonucleoprotein La.A - African clawed frog
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence revision 26-May-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
(;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb_194 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: S33817; S28544
R;Scherly, D; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33817; MUID:93287095; PMID:8510143
A;Accession: S33817
A;Molecule type: mRNA
A;Residues: 1-427 <SCH-
A;Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876
C;Comment: This protein associates with a variety of small RNA molecules, most of whay act as a transcription termination factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ay act as a transcription termination factor.

()Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

()Keywords: phosphoprotein; RNA binding

F;112-178/Domain: ribonucleoprotein repeat homology <RRM>

F;113-118/Region: RNA-binding RNP2 motif

F;151-158/Region: RNA-binding RNP1 motif
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A;Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection A;Reference number: JC1494; MUID:93246255; PMID:7916708
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A; Residues: 1-415 < SEM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology; Keywords: phosphoprotein; RNA binding; keywords: phosphoprotein; RNA binding; keywords: ribonucleoprotein repeat homology <RRM>
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                                                                                                                                                                                                                              12
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735	696	631	529	506	505	487	461	390	390	388	346	183	166	104	503	
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T41187	F83886	S36505	T00677	F85016	B90181	T27653	T27651	A53781	A53773	AF0183	A82659	B29017	T32701	CCRD2	JN0524	
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ALIGNMENTS

A31888 ribonucleoprotein La - human ribonucleoprotein La - human ribonucleoprotein La - human N,Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antige C;Species: Homo sapiens (man) C;Date: 21-May-1990 #sequence revision 26-May-1994 #text_change 22-Jun-1999 C;Date: 21-May-1990 #sequence revision 26-May-1990 #sequence domains of the human La autoantigen A;Tetle: Genomic structure and amino acid sequence domains of the human La autoantigen A;Accession: A31888 A;Accession: A31888 A;Accession: A31888 A;Accession: A31888 A;Chan; A;Chan; A;Chan; A;Chan; B;Chan; B;	Query Match 88.8%; Score 87; DB 1; Length 404; Best Local Similarity 83.3%; Pred. No. 3.7e-,07; Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 1 AALQAKICHQIQYYFGQF 18 :	A;Molecule type: mRNA A;Residues: 1-404 < CHA> A;Residues: 1-404 < CHA> A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Note: part of this sequence was confirmed by protein sequencing C;Comment: This protein associates with a variety of small RNA molecules, most of which ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: blocked amino end; phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology < RRM> F;113-118/Region: RNA-binding RNP2 motif F;151-158/Region: RNA-binding RNP1 motif F;228-404/Domain: phosphorylated #status predicted < PHY>	RESULT 1 S03849 ribonucleoprotein La - bovine ribonucleoprotein SS-B N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Bos prindjenius taurus (cattle) C;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999 C;Acc:sssion: S03849 R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989 A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences A;Reference number: S03848; MUID:89202037; PMID:2468131 A:Accession: S03848 MUID:89202037; PMID:2468131

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative GntR-family regulatory protein.
VPA1237.

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RESULT 15
Q9LJ02
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                                                                                                                                                             T Clone:p10499C11.";

I clone:p10499C11.";

I Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; APO01080; BAA90356.1; -.

R Gramene; Q9LJ02; -.

R Gramene; Q9LJ02; -.

R InterPro; IPR006630; Lupus_La_dom.

Pfam; PF05383; La; 1.

Pfam; PF05383; La; 1.

SMART; SM00684; DM15; 3.

DR SMART; SM00684; DM15; 3.

DR SMART; SM00684; DM15; 3.

SNART; SM00715; LA; 1.

SQ SEQUENCE 928 AA; 103745 MW; 53FC46E24A446EB4 CRC64;
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Best Local S
Matches 7
                                                                                    Query Match
Best Local S
Matches 10
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EMBL; AP005088; BAC62580.1; -. EMBL; AP005088; BAC62580.1; -. GO; GO:0003700; F.transcription factor activity; IEA. GO; GO:0005622; C.:intracellular; IEA. GO; GO:0003755; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 478 AA;
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Pfam; PF00392; gntR; 1.
PRINTS; PR00035; HTHGNTR.
PROSITE; PS00043; HTH_GNTR_FAMILY; 1.
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STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739;
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Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LJ02;
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBI_TaxID=4530;
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                                                                                    l Similarity
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LEAQICQQIEYYF-GD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QICQQIEYYFGD
                                                                                 47.4%; Score 45.5; ilarity 62.5%; Pred. No. 73; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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묽 278 LRAKILTQVEYYFSGD 293

Search completed: September 10, 2004, 17:59:59 Job time: 44.229 secs

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RESULT 12
Q9FL36
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Matches
Query Match
Best Local Similarity
                                                                                                                           InterPro; IPR002344; Lupus_La.
InterPro; IPR00630; Lupus_La.
InterPro; IPR00630; Lupus_La.
InterPro; IPR006504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
PFRNTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA. GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA. InterPro; IPR003331; Epimerase 2. Pfam; PF02350; Epimerase 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last samotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similarity to RNA-binding protein.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).
EMBL; AP003358; BAB56326.1;
EMBL; AP003129; BAB41379.1;
                                                                                                                                                                                                                                                                                                                                                                                               physically assigned P1 and TAC clones.";
DNA Res. 5:131-145(1998).
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HSSP; P27828; 1F6D.
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TIGRFAMs; TIGR00236; wecB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structural analysis of Arabidopsis thaliana chromosome features of the regions of 1,381,565 bp covered by twent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Columbia;
MEDLINE=98344145;
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GO:0005634; C:nucleus; IEA.
GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TaxID=3702;
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391 AA;
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                                                                                                          PS50102; RRM;
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ilarity 72.7%;
Conservative
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                                                                                  45655 MW;
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  49.0%;
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  Score
Pred.
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                                                                               A2EF62EB5B89B099 CRC64;
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  47;
No.
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RESULT
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Q94A38;
Q1-DEC-2001
01-DEC-2001
01-OCT-2003
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Q87GS8;
Q87GS8;
01-JUN-2003
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Shinn P., Chen H., Carninci P., Dale J.M., Goldsmith A.D.,
Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick /
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
"Arabidopsis cDNA clones."
"Arabidopsis cDNA clones."
                                                                                                                                                                                                           PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                   GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002344; Lupus_La_
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
Dfam. DF051321; ro. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Chan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., W. Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis J.
                                                                                                                                                                                                                       PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       "Arabidopsis ORF clones.",
Submitted (SEP-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
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                                                                                                                                                    Similarity 53...
8; Conservative
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(TremBLrel. 25, Last ann
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                                                                                                                                                                 49.0%;
                                                                                                                                                                                                              46842 MW;
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(TrEMBLrel. 24,

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RESULT 10
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P72382
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Best Local S
Matches
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EMBL, AP004822; BAB94004.1; -.

GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;

GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.

GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.

InterPro; IPR003331; Epimerase_2.

InterPro; IPR003331; Epimerase_2.
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01-FEB-1997
01-JUN-2003
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  P95709
P95709;
                                                                                                                                                                                                                                                                                                             Pfam; PF02
TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sau S., Sun J., Lee C.Y.;
"Molecular characterization and transcriptional analysis capsule genes in Staphylococcus aureus.";
J. Bacteriol. 179:1614-1621(1997).
EMBL; U73374; AAB49445.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired MRSA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96178981; PubMed=8606192;
Sau S., Lee C.Y.;
"Cloning of type 8 capsule genes and analysis of production of different capsular polysaccharides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
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Pfam; PF02350; Epimerase_2; 1.
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GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
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8; Conser
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                                                                                                                                                                OICQQIEYYFG 16
                                                                                                                                                                                                                                                                                       2350; Epimerase 2; 1.
TIGR00236; wecB; 1.
391 AA; 44247 MW;
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(TrEMBLrel.
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                     PRELIMINARY;
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72.7%;
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Pred.
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Mismatches
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RESULT 11
Q99X57
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Matches 8
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Q99X57;
01-JUN-2001
01-JUN-2001
01-JUN-2003
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01-MAY-1997
01-JUN-2003
                                                                             099X57;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Capsular polysaccharide synthesis enzyme Cap5P.
CAPP OR SAVO164 OR SA0159.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315).
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TIGRFAMs;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Reynolds and Newman;
Bagga N., Wann E.R., Foster T.J., Lee J.C.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U81973; AAC46099.1;
EMBL; U81973; AAC46099.1;
EMSP; P27828; 1F6D.
GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity;
GO; GO:0009103; P:UDP-N-acetylglucosamine metabolism; IEA.
GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Reynolds and Newman;
MEDLINE=98125727; PubMed=9466251;
Massin N., Albus A., Michon F., Livolsi P.J., Park J.-S
"Identification of a gene essential for O-acetylation o
Staphylococcus aureus type 5 capsular polysaccharide.";
Mol. Microbiol. 27:9-21(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Reynolds and Newman;
MEDLINE=9738857; PubMed=9245821;
Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.
"The Staphylococcus aureus allelic genetic loci for serotype
capsule expression contain the type-specific genes flanked by
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                                                                    Staphylococcus aureus (strain N31)
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Staphylococcus aureus cap50 and cap5P mutations affecting enterobacterial com Escherichia coll.";
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                                           NCBI_TaxID=158878,
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PF02350; Epimerase_2; 1.
AM8; TIGR00236; wecB; 1.
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                                                                                                                                                                                                                                                                                   PRELIMINARY;
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72.7%;
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Pred. No.
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5.4;
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PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1
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Q7ZTIO;
01-JUN-2003
01-JUN-2003
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SEQUENCE FROM N.A.

SEQUENCE FROM N., Brokstein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,

Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,

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Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,

Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,

Miranda A., Miranda A., Mungall C.J., Paragas V., Paragas V., Paragas V., Paragas V
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01-JUN-2002
01-OCT-2003
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                                                                                                                     Submitted (JAN-2002) to the EMBL/Ge
EMBL; AY075257; AAL68124.1; -.
FlyBase; FBBn0011638; La.
GO; GO:0008098; F:5S rRNA primary t
GO; GO:0003723; F:RNA binding; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Inso
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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LA OR CG10922.
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                             InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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2 (TrEMBLrel.
3 (TrEMBLrel.
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Erel. 24,
Erel. 25,
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Pred. No.
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annotation
                                                                                                                                                             transcript
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Best Local S
Matches 9
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PRINTS; PR00302; LUPUSIA.

SMART; SM00715; LA; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM RNP_1; 1.

PROSITE; PS00030; RRM RNP_1; 1.
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Best I
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund
Saski C., Henry D., Oates R
"Rice Genomic Sequence.";
Submitted (JUN-2002) to the
                                                                                                               Q8NYN8 PRELIMINARY;
Q8NYN8;
01-OCT-2002 (TrEMBLrel. 2
01-OCT-2002 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22040717; PubMe
Baba T., Takeuchi F., K
Baba T., Takeuchi F., K
Nagai Y., Iwama N., Asa
Yamamoto K., Hizamatsu
"Genome and virulence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
OSJNBA0011114.12.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, En
Spermatophyta, Magnoliophyta, Liliopsida,
Ehrhartoideae, Oryzeae, Oryza.
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Gramene; Q8LMP9; -.
InterPro; IPR006630; Lupus_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBLMP9;
                                                               Staphylococcus aureus Bacteria; Firmicutes; NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 48
                                                                                                                                                                                                                                                                                                  InterPro; IPR006630; Lupus_La_dom
Pfam; PF05383; La; 1.
SMART; SM00715; LA; 1.
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                                                                                              Capsular polysaccharide CAPSP OR MW0139.
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     rakeuchi F., Kuroda M.,
Iwama N., Asano K., Na.
K., Hiramatsu K.;
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                                                                                                                                                                                                                                                                                 481 AA;
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                                     PubMed=12044378;
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Bacillales;
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Mismatches
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a; Poales; Poaceae;
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                   H., Aol
Kuroda
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                  Aoki K.
oda H.,
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                   K.-I.,
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RESULT 3
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Best Local S
Matches 15
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Best Local S
Matches 15
                                                                                                                                                                                                                                                     MGD; MGI:98423; Ssb.
GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR003244; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF05383; La; 1.
Pfam; PF00076; xrm; 1.
PRINTS; PR00305; LUPUSLA.
SMART; SM00715; LA; 1.
SEQUENCE 381 AA; 43891 N
             Q8QHI5;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8BTU4
Q8BTU4;
                                                                                                                                                                                        PRINTS; PR00302; LÜPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; 1.
SEQUENCE 415 AA; 47657 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research "Analysis of the mouse transcriptome b 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sjogren syndrome antigen
                                                      Q8QHI5
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
                                                                                                                                                                                                                                                                                                                             EMBL; AK088677; BAC40498.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
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                                                                                                                           2 ALEAQICQQIEYYFGDF 18
                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALEAKICHQIEYYFGDF 28
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3 (TrEMBLrel. 23,
3 (TrEMBLrel. 25,
ndrome antigen B.
(TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
region binding protein.
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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                                                                                                                                                          86.5%;
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88.2%;
                                                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                 Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83; DB 11;
Pred. No. 1.7e-05;
                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2E2DEF1452C0F0E9 CRC64;
                                                                                                                                                                                          A7545C7686AC8363 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                 Mismatches
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based on functional
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                                                       206
                                                                                                                                                            1.9e-05;
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annotation
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LDTKICEQIEYYFGD

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RESULT 4
Q7ZTK2
ID Q7ZT
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                                                                                    Query Match
Best Local S
Matches 11
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Best Local S
Matches 12
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SMART; SM00715; LA; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM RNP_1; 1.

SEQUENCE 206 AA; 23992 MW; 96
                                                                                                                                                                                                                                                                 Pfam; PF00076; rrm; 1.

PRINTS; PR00302; LUPUSLA.

SMART; SM00715; LA; 1.

SMART; SM00360; RRM; 2.

PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7ZTK2;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Similar to lupus LA protein homolog B.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UBP.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aichosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Strausberg R.;

Submitted (FEB-2003) to the EMB

EMBL; BC046654; AAH46654.1; -.

GO; GO:0005534; C:nucleus; IEA.

GO; GO:0003723; F:RNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L'Ecuyer T.J., Fang H.-L.;
Submitted (JAN-2002) to the EMB:
EMBL; AF467897; AAL76269.1; -
GO; GO:0005534; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7ZTK2
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Pfam; PF00076; rrm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002344; Lupus_La_dom.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
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                                                                                                                           Similarity
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LEAQICQQIEYYFGD
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                                                                                            Conservative
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                                                                                                                                                                                                                                      48996 MW;
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; Pred. No. .
                                                                                    Score 68; DB Pred. No. 0.00 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427
                                                                                                                           DB 13;
0.006;
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ia; Pipoidea; Pipidae;
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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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Perfect score:
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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96
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137.751 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1017041 seqs, 315518202 residues
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_vartebrate:*
sp_virus:*
sp_vertebrate:*
sp_virus:*
sp_vartebrate:*
sp_vartebrate:*
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                                                                                                                                                                                                                                          human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score 83	24 CF		DB 11	ID Q9CYB9
ν ⊦	83 6	86.5 5	415	11	Q8BTU4
ω	70	72.9	206	13	Q8QHI5
4	89	70.8	427	13	Q7ZTK2
σ	60	62.5	401	13	Q7ZTI0
თ	52	54.2	390	ഗ	Q8T8V5
7	52	54.2	481	10	Q8LMP9
œ	50	52.1	381	16	Q8NYN8
9	50	52.1	391	N	P72382
10	50	52.1	391	N	P95709
11	50	52.1	391	16	Q99X57
12	47	49.0	411	10	Q9FL36
13	47	49.0	422	10	Q94A38
14	47	49.0	478	16	Q87GS8
15	45.5	47.4	928	10	Q9LJ02
16	45	46.9	396	'n	001806

44 45	43	42	41	40	39	38	37	36	35	ب 4.	ω ω	မ သ	31	3 0	29	28	27	26	25	24	23	22	21	20	19	18	17
42 42	42	42	42	42	42	42	42	42	42	42	42	42	43	43	43	43	43	43	43	43	44	44	44	44	44	45	45
43.8 43.8		43.8		43.8		43.8			43.8	•	43.8							44.8		44.8	45.8	45.8	45.8			46.9	46.9
965 1064	669	575	482	482	342	328	269	239	214	186	159	151	545	506	355	271	181	119	111	91	1126	1126	898	506	389		883
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Q9VAW5 Q8FUH0	Q8XRQ1	Q8NAF2	Q8G0Z3	Q8YGX0	Q9CUQS	Q9NW12	Q8MYR3	Q9P8N6	Q9CSI2	Q8VDW3	Q97LL1	Q86MR7	080567	Q84TQ4	Q8RYB4	Q82FZ4	Q82Z79	Q9ZP89	Q978R4	044678	Q7YXY0	Q86PR0	Q8LRF3	Q9M143	BT0S8Q	Q940X9	Q9VBE6
Q9vaw5 drosophila Q8fuh0 corynebacte	ral		bru.		mus	Q9nw12 homo sapien	Q8myr3 drosophila	Q9p8n6 cochliobolu	Q9csi2 mus musculu	mus		יטי			Q8ryb4 phytophthor		Q82z79 enterococcu	Q9zp89 neurotheca	Q978r4 thermoplasm	044678 caenorhabdi		Q86pr0 cryptospori	Q81rf3 oryza sativ	arabidops		arabidops	

ALIGNMENTS

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SEQUENCE FROM N.A. SEQUENCE FROM N.A. SETRAIN=C57BL/60; TISS MEDLINE=2108560; Pub Kawai J., Shinagawa A Arakawa T., Hara A., Aizawa K., Izawa M., Salto T., Okazaki Y., Salto T., Okazaki Y., Salto T., Okazaki Y., Salto T., Dewis S., M Schriml L.M., Staubli Sakai K., Okido T., Blake J., Boffelli D. Brownstein M.J., Bult Guoris P., Marchionni Nordone P., Ring B., Sasaki H., Sato K., Sasaki H., Sato K., Sasaki H., Sato K., Sasaki H., Toyo-oka K Wynshaw-Boris A., Yos "Hunctional annotatio Nature 409:685-690(20 EMBL; AK017822; BAB30 MGD; MGI:98423; Ssb.	HT 1 B9 Q9CYB9; Q9CYB9; O1-UN-2001 (TrEMBLz O1-OCT-2003 (TrEMBLz O1-OCT-2003 (TrEMBLz S)Gyren syndrome ant SSB. Mus musculus (Mouse) Eukaryota; Metazoa; Mammalia; Eutheria; NCBI TaxID=10090;
SEQUENCE FROM N.A. STRAIN=CS7BL/GJ; TISSUB=Embryo; STRAIN=CS7BL/GJ; TISSUB=Embryo; MEDLINE=20185660; PubMed=11217851; Yoshino M., Kawai J., Shihagawa A., Shibata K., Yoshino M., Arakawa T., Hara A., Fukunishi Y., Konno H., Kan Arakawa T., Hara A., Fukunishi Y., Konno H., Kan Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kon Saito T., Okazaki Y., Gojobori T., Bono H., Kan Yeleischmann W., Gaasterland T., Gissi C., King Kadota K., Matsuda H.A., Ashburner M., Batalov Fleischmann W., Gaasterland T., Gissi C., King Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peso Schriml L.M., Staubli F., Suzuki R., Tomita M., Sakai K., Okido T., Furuno M., Aono H., Baldare Blake J., Boffelli D., Bojunga N., Carninci P., Brownstein M.J., Bult C., Fletcher C., Fujita M. Gustincich S., Hill D., Hofmann M., Hume D.A., Lyons P., Marchionni L., Mashima J., Mazzarelli Nordone P., Ring B., Ringwald M., Rodriguez I., Sasaki H., Sato K., Schoenbach C., Seya T., Shi Sasaki H., Sato K., Wang K.H., Weitz C., Wh Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wh Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wh Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wh Hayashizaki Y., "Functional annotation of a full-length mouse C Nature 409:685-690(2001) EMBL; AK017822; BAB30957.1; -	T 1 9 9 9 9 QOCYBB PRELIMINARY; QOCYBB; (01-JUN-2001 (TrEMBLrel. 17, C 01-JUN-2001 (TrEMBLrel. 21, L 01-OCT-2003 (TrEMBLrel. 25, L 01-OCT-2003 (TrEMBLrel. 26, L 01-OCT-2003 (TrEMBLrel. 27, L 01-OCT-2003 (TrEMBLrel. 17, C 01-JUN-2001 (TREM
gall17851; Yoshino lakunishi Y., Konno H., Ishi K., Kiyosawa H., Ishi K., Kyosawa H., Jobobri T., Bono H., Jobobri T., Bono H., Jobobri T., Bono H., John T., Gissi C., Ki fand T., Gissi C., Ki fand T., Gissi C., Ki fand T., Gissi C., Firmino M., Aono H., Bald Bojunga N., Carninoi C., Fletcher C., Fujit Hofmann M., Hume D.A., Mashima J., Mazare hoenbach C., Seya T., Wang K.H., Weitz C., Wang K.H., Weitz C., Wang K.H., Weitz C., Wang K.H., Hasegawa Y., Kida K., Hasegawa Y., Kida K., Hasegawa Y., Kof a full-length mous D.	ดิ ดิ 🗟
Itoh M., Ishiachi, Fukudado S., Yamanakado S., Yamanakado S., Casavant T., Saitt S., Casavant T., Kochiwa H., Kochiwa H., Gariboldi M., Lee J., Mombaerts Sakamoto N., Storolittaker.C., Wiji H., Kohtsuk.	AA. update) on update) ertebrata; Euteleost i; Muridae; Murinae;
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SRO9_YEAST
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Matches 6
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P25567;
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"AtVPS45 c:
Mol. Biol.
-!- FUNCTI
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EMBL; AC004260; AAC34344.1; -.
EMBL; AC050370; AAX591388.1; -.
EMBL; AY101517; AAM26638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=20346955; PubMed=10888666;
                           MEDLINE=98043396; PubMed=9383048; Kagami M., Toh-E A., Matsui Y.; Watsui Y.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
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organization of the actin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; T00445; T00445.
PIR; T52056; T52056.
                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                      Delgado M., Esteban M.,
Submitted (MAR-1992) to
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SIMILARITY: Belongs to the STXBP/UNC-18/SEC1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cis-Golgi with SYP31.
SUBCELLULAR LOCATION: Peripheral membrane protein. Binds to trans-
SUBCELLULAR LOCATION: Peripheral membrane protein with other proteins.
Solai network membranes through interaction with other proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Involved in the protein transport to the vacuole, probably at the level of vesicle fusion at the trans-Golgi network (TGN) and not in transport from the TGN to the prevacuolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   compartment. Binds syntaxins.
SUBUNIT: Interacts with both SYP41 or SYP42 and VTI12, ldifferent domains of the trans-Golgi network. Does not the pervacuolar compartment with VTI11, SYP21 or SYP22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Golgi network membranes through interaction with other proteins. TISSUE SPECIFICITY: Highly expressed in roots, lower expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
OR YCL037C OR YCL37C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                          Navas L.;
the EMBL/GenBank/DDBJ databases
   cytoskeleton.";
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Pred. No. 9.8;
5; Mismatches
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GO; GO:0005844; C:polysome; IDA.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0006412; P:protein biosynthesis;
InterPo; IPRO6630; Lupus_La_dom.
Pfam; PF05383; La; 1.
SMART; SM00715; LA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its monoperofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -.- FUNCTION: May overlap in function with tropomyosin and involved in organization of actin filaments. Acts as a suppressor of RHO3.
-!- SIMILARITY: Some, to yeast SLF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics 147:1003-1016(1997).
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DOMAIN
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       297
                                                                              7 ICQQIEYYFGD 17
                                                                                                                                                Similarity 63.07; Conservative
| :||||| :
|ARQIEYYFSE
                                                                                                                                                                                                                                                                                                    466 AA;
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                                                                                                                                                                                                                                                                                                        51789
       307
                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                       Score 41;
Pred. No.
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POLY-ASN.
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18;
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                                                                                                                                                                                                                          1; Length 466;
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Search completed: September 10, 2004, 17:53:02 Job time : 10.2402 secs

VARIANT GALACTOSEMIA THR-28

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   InterPro; IPR000705; Galactokinase.
InterPro; IPR00174, Galkinase.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR006203; GHMPkinase.
InterPro; IPR006203; GHMPkinase.
InterPro; IPR006206; Mev_galkinase.
Pfam; PF00288; GHMP kinases; 1.
PRINTS; PR00473; GALCTOKINASE.
PRINTS; PR00959; MBYGALKINASE.
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Kalaydjieva L., Perez-Lezaun A., Angelicheva D., Onengut
Bosbhard N.U., Jordanova A., Savov A., Yanakiev P., Krem
Radeva B., Hallmayer J., Markov A., Nedkova V., Tournev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U26401; AAA96147.1; -.
EMBL; L76927; AAB51607.1; -.
EMBL; BC001166; AAH01166.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT GALACTOSEMIA VAL-198.
MEDLINE=21152290; PubMed=11231902;
Okano Y., Asada M., Fujimoto A., Ohtake A., Murayama K., Hsiao K.-J.,
Choeh K., Yang Y., Cao Q., Reichardt J.K.V., Niihira S., Imamura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0004335; F:galactokinase activity;
GO; GO:0006012; P:galactose metabolism; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Major enzyme for galactose metabolism.
-!- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characterization
                                                SEQUENCE
                                                                                                                            VARIANT
                                                                                                                                                            NP_BIND
VARIANT
                                                                                                                                                                                                       TIGREAMS; TIGRO0131; gal kin; 1.

PROSITE; PS00106; GALACTOKINASE; 1.

PROSITE; PS00627; GHMP KINASES ATP; 1.

Transferase; Kinase; Galactose metabolism; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 604313;
MIM; 230200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic factor for age-related cataract: identification and aracterization of a novel galactokinase variant, 'Osaka,' in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     founder mutation in the GK1 gene is responsible for galactokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate.

PATHWAY: Galactose metabolism; first step.

DISEASE: Defects in GALKI are the cause of galactosemia II

DISEASE: Defects in GALKI are the cause of galactosemia II

[MIM:230200], an autosomal recessive deficiency characterized be congenital cataracts during intancy and presenile cataracts in adult population. The cataracts are secondary to accumulation c galactitol in the lenses.

SIMILARITY: Belongs to the GHMP kinase family. GalK subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:4118; GALK1.
                                                                                                                                                                                            mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in Roma (Gypsies).";
. Genet. 65:1299-1307(1999)
                                    392
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                                                                                              198
                                                A,
                                                                                                                                                          144
28
                                                                                              198
                                                                                                                           32
                                                42272 MW;
 45.8%;
57.1%;
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                                                                                                                                                              ATP
                                                                                                            /FTId=VAR_008514.
V -> M (in galactosemia II).
/FTId=VAR_002547.
 Score 44;
Pred. No.
                                              A -> V (in galactosemia II; mild deficiency; Osaka).
/FIId=VAR 015746.
8D7CFF8FDB0E4718 CRC64;
                                                                                                                                                              (in galactosemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
 DB
4.3;
                1;
              Length 392
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RESULT VP45 ULT VP45 
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RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RX Theologis A., Altasi H., Araujo R., Bowman C.L., Brooks S.Y.,
RX Mhite O., Alonso J., Altasi H., Cheuk R.F., Chin C.W.,
RX Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RX Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RX Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RX Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RX Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RX Chung M.K., Conn L., Conway A.B., Conway A.R., Fong B., Fujii C.Y.,
RX Chung M.K., Conn L., J., Feng J.-D., Fong B., Fujii C.Y.,
RX Chung M.F., Coldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RX Chin J.E., Goldsmith A.D., Johnson-Hopson C., Khan S., Khaykin E.,
RX Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RX Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RX Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RX Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RX Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RX Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RX Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RX Militscher J., Miranda M., Nguyen M., Roney T., Rowley D.,
RX Militscher J., Tambunga G., Toriumi M.J., Town C.D.,
RX M. Lin X., Yun Aken S., Vuysberg M., Vysotskaia V.S., Walker M.,
RX Mu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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ARATH
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O49048; O806
28-FEB-2003
                                                                                                                                 Yamada K., Lim J. Dale J.M., Chen H., Shinn P., Palm C.J.,
Yamada K., Lim J. Dale J.M., Chen H., Shyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
Juan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 42, Last annotation update)
Vacuolar protein-sorting protein 45 homolog (AtVPS45
VPS45 OR AT1G77140 OR T14N5_2.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=98289086; PubMed=9625693;
Bassham D.C., Raikhel N.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22954850; PubMed=14593172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence and thaliana.";
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INTERACTIONS WITH SYP21; SYP22; SYP31; SYP41; SYP42; SYP61; VTI11 AND
                                                                        Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:816-820(2000).
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                                                                            302:842-846(2003).
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RESULT 12
GAL1_CANFA
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Best Local
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                                                                                                                                          EMBL; AF213513; AAG43832.1; -.
EMBL; AF24963; AAG15527.1; -.
EMBL; AY267338; AAP31026.1; -.
InterPro; IPR000705; Galactokinase.
InterPro; IPR0001174; Galkinase.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR006203; GHMPkinse ATP.
InterPro; IPR006204; Mev galkinase.
Pfam; PF00288; GHMP kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Major enzyme for galactose metabolism.
-!- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-gala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                PRINTS; PR00473; GAĪCTOKINASE.
PRINTS; PR00960; LMBPPROTEIN.
PRINTS; PR00959; MEVGALKINASE.
TIGRFAMS; TIGR00131; gal kin; 1.
PROSITE; PS00106; GALACTŌKINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22508185; PubMed=12620391; Sidjanin D.J., Miller B., Kijas J., McElwee J., Pillardy J., Malek J., Pai G., Feldblyum T., Fraser C., Acland G., Aguirre G.; Pai G., Feldblyum T., Fraser C., Acland G., Aguirre G.; Pasi G., Patter G., Acland G., Aguirre G.; Pasi G., Pas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galactokinase
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                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graves K.T., Ennis R.B.;
"Exon scan of the canine galactokinase (GALK1)
affected with juvenile cataract.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALKI.

Canis familiaris (Dog).

Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last seq
15-MAR-2004 (Rel. 43, Last ann
3alactokinase (EC 2.7.1.6) (Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    idjanin D.J.;
Identification and
                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute. The by non-profit institutions as long lifted and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEC-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galactose metabolism; first step.
TY: Belongs to the GHMP kinase family. Galk subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
GHMP_KINASES_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis of canine galactokinase (GALK1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54571 MW;
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annotation update)
(Galactose kinase)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7D4E0EE7760A0AF7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no resuong as its content
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A Klausner R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Best Local
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P51570;
               Ai Y., Basu M., Bergsma D.J., Stambolian D.;
"Comparison of the enzymatic activities of human galactokinase and a related human galactokinase protein GK2.";
Pincham Biophys. Res. Commun. 212:687-691(1995).
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NP_BIND 134 144 ATP (POTENTIAL)
SEQUENCE 392 AA; 42120 MW; 8FD5ECF3AB431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97064967; PubMed=8908517;
Bergsma D.J., Ai Y., Skach W.R., Nesburn van Horn S., Stambolian D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALK1 OR GALK.
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01-OCT-1996 (Rel. 34, Last
10-OCT-2003 (Rel. 42, Last
Galactokinase (EC 2.7.1.6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6:980-985(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                        MEDLINE=95352063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Fine structure of the human galactokinase GALK1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of the galactokinase cDNA and identification of mutations :wo families with cataracts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bergsma D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95400298;
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                                                                                                                                              PubMed=7542884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., AND VARIANT GALACTOSEMIA MET-32
PubMed=7670469;
Y., Sidjanin D., Nesburn K., Sath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
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(Galactose kinase)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nesburn K., Sathe G., Rosenberg M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392
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                                                                                      GALK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.W.,
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ENDER REPORT OF THE PROPERTY O
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TCMO_PETCR
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Best Local
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15-DEC-1998
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petroselinum crispum (Parsley) (Petroselinum hortense).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

campanulids; Apiales; Apiaceae; Apioideae; apioid superclade;

Apium clade; Petroselinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic a 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; FALSE_NEG
RNA-binding; Nuclear protein.
DOMAIN 154 236 RNA-BINDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00302; LUPUSLA. SMART; SM00715; LA; 1. SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000504; I
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GeneDB SPombe; SPAC57A10.10c; -.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Logemann E., Parniske M., Hahlbrock K:;
"Modes of expression and common structural features of the phenylalanine ammonia-lyase gene family in parsley.";
Proc. Natl Acad. Sci. U.S.A. 92:5905-5909(1995).
-I- FUNCTION: Controls carbon flux to pigments essential
                                                                                                                                                                                                                        modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM

    -!- PATHWAY: Lignin biosynthesis.
    -!- PATHWAY: Phenylpropanoid metabolism; second step.
    -!- SIMILARITY: Belongs to the cytochrome P450 family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYP73A10 OR CYP73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                      EMBL; L38898; PIR; T14907; '
                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. Th
Oxidoreductase; Monooxygenase; Heme; NADP
                                                                        InterPro; IPR001128; Cytochrome_P450
Pfam; PF00067; p450; 1.
                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    modified and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pollination or UV protection, to numerous pytoalexins s by plants when challenged by pathogens, and to lignins. CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-hydroxycinnamate + NADP(+) + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T43542; T43542
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                                                PR00385; P450
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                            PS00086;
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298 AA;
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                                                                                                                         T14907
                                                                                                                                                  AAC41660.1;
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                            CYTOCHROME P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
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                                                                                                                                                                                                                     license agreement (See http://www.isb-sib.ch/announce,
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50.0%;
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M -> I (IN REF.
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Pred. No. 0.42;
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                       EMBL; AE016995; AAP05038.1; -.
TIGR; CCA00289; -.
HAMAP; MF 00121; -; 1.
InterPro; IPR004413; GatB.
InterPro; IPR006107; GatB cent.
InterPro; IPR006075; GatB N.
InterPro; IPR0030789; GatB_Yqey.
Pfam; PP01162; GatB, 1.
Pfam; PP02637, GatB N; 1.
PROSITE; PS01234; GATB; 1.
PROSITE; PS01234; GATB; 1.
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IO-OCT-2003 (Rel. 42, Last annotation update)
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit
(EC 6.3.5.-) (Asp/Glu-ADT subunit B).
GATB OR CCA00289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Some send an email to license@isb-sib.ch).
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-!- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-GPIC;
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examining the role of niche-specific genes in the evolution c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22569155; PubMed=12682364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial inficiency in the statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine + phosphate + L-glutaminyl-tRNA(Gln) + L-glutamate - CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(Asn) + L-glutamine + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate + L-glutamine + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamine + phosphate + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamine + phosphate + pho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases. The reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily
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and this statement
requires a license
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50.0%;
   Ligase; Complete proteome
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Pred. No.
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; 32F00EE959D69CCF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             moved. Usage by and for commercial (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Mornis J., McSherfi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mornis J., McSherfi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeng X.H., Zhong F. M., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F. M., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
RT "The genome sequence of Drosophila melanogaster.";
CC polymerase III Binds RNA and DNA. Binds to precursors of RNA
polymerase III transcripts. May play a specialized role during fly
                                                                                                      Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U07652; AAA20518.1; -.
EMBL; L32988; AAA21776.1; -.
EMBL; AE003666; AAF53885.1; -.
EMBL; A53773; A53773.
PIR; A53781; A53781.
                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0011638; La.
GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.
GO; GO:0003723; F:RNA binding; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; :
RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glands.
SIMILARITY: Contains 1 RNA recognition motif SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo followed by a restricted pattern of mesodermal expression that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              later confined to the visceral mesoderm,
51
                                                4
                                                                                                      Similarity 9; Conserv
ERAIIRQVEYYFGD 64
                                                EAQICQQIEYYFGD 17
                                                                                                                                                                                                            169
182
283
329
                                                                                                      Conservative
                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                        234
169
183
283
329
                                                                                                                                                                                                                 44884
                                                                                                                               54.2%;
                                                                                                                                                                                                                                                                                           RNA-BINDING (RRM).

A -> T (IN REF. 1).

KH -> NS (IN REF. 1)
                                                                                                                            Score 52;
Pred. No.
                                                                                                                                                                                                                                        A -> R (IN REF. 1).
K -> N (IN REF. 1).
                                                                                                                                                                                                               A8099288B90446A5 CRC64;
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                      DB_1; Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gonads, gut, and
                                                                                                                                                                                                                                                                                              1).
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MBL outstation -
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RX. MEDLINE=21848401; PubMed=11859360;
RX MEDLINE=21848401; PubMed=11859360;
RA Sgouros J., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peatr N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gollins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Raylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Benito J.,
RA Golfeau A., Cadieu E., College G., Ra, Moore G., Ra, Moore G., Ra, Moore G., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 41, Last annotation update)
La protein homolog (La ribonucleoprotein) (La SLAI OR SPAC57A10.10C.
EMBL; AF022949; AAB82145.1; -.
EMBL; AB011371; BAA24981.1; -.
EMBL; Z94864; CAB08173.1; -.
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Binds to the precursors of poly Functions in tRNA maturation.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
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MEDLINE=98067398; PubMed=9404894;

WEDLINE=98067398; PubMed=9404894;

Van Horn D.J., Yoo C.J., Xue D., Shi H., Wolin S.L.;

Van Horn D.J., Yoo C.J., Xue D., Shi H., Wolin S.L.;

"The La protein in Schizosaccharomyces pombe: a conserved yet dispensable phosphoprotein that functions in tRNA maturation.";

RNA 3:1434-1443(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 RNA recognition motif (RRM) domain. SIMILARITY: TO VERTEBRATE PROTEIN LA.
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RESULT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM RNP 1; 1.

RNA-binding; Nuclear protein; Phosphorylation.

RNA-binding; Nuclear protein; Phosphorylation.

DOMAIN 111 203 RNA-BINDING (RRM)

DOMAIN 196 212 NUCLEAR LOCALIZAT

DOMAIN 316 332 NUCLEAR LOCALIZAT

DOMAIN 316 332 NUCLEAR LOCALIZAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002344;
InterPro; IPR006630;
InterPro; IPR000504;
                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aec NCBI_TaxID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1
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                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restructed the succession of the successio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     La protein homolog (La ribonucleoprote
Aedes albopictus (Forest day mosquito)
                     Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                              InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                    EMBL; S80954; AAB35931.1; -.
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                     amounts are present in the cytoplasm. SIMILARITY: Contains 1 RNA recognition motif SIMILARITY: TO VERTEBRATE PROTEIN LA.
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PR00302; LUPUSLA
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41, Last annotation update)
g (La ribonucleoprotein) (La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Lupus_La.
; Lupus_La_dom.
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71.4%;
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NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL NUCLEAR LOCALIZATION SIGNAL AEB3A38B7DZE3EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 64; I
Pred. No. 0.
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                                                                                                                                                                                                        noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
0.0014;
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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Barel R.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Genson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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SMART; SM00360; RRM; 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; FALSE NEG.
RNA-binding; Nuclear protein; DNA-binding.
RNA-BINDING; NAS-BINDING; NAS-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo:
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P40796; Q24375; Q9VIN2;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LA_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Canton-S; TISSUE=Ovary;
MEDLINE=94309632; PubMed=8035794;
Bai C., Li Z., Tolias P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Canton-S; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
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LA OR CG10922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins from Drosophila melanogaster and Saccharomyces evisiae: a yeast homolog of the La autoantigen is dispensable
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Cell. Biol. 14:5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homolog
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Pred. No. 0.032;
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RESULT 5
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01-AUG-1992
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between
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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR00630; Lupus La.
dom.
InterPro; IPR000504; RNA_rec_mot.
pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                expression.";
J. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93287095; PubMed=8510143; Scherly D., Stutz F., Lin-Marq N., Clarkson S.G.; "La proteins from Xenopus laevis. cDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-AUG-1992 (Rel. 23, Created)
Ol-AUG-1992 (Rel. 23, Last sequence
15-MAR-2004 (Rel. 43, Last annotatic
Lupus La protein homolog B (La ribor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. 231:196-204(1993).
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                                                                PTM: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of I
SIMILARITY: HIGH, TO MAMMALIAN LA PROFI
SIMILARITY: Contains 1 RNA recognition
                                                                                                                                                                                                 FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3 termini of virtually all mascent polymerase III transcripts (By similarity).

SUBCELLULAR LOCATION: Nuclear (Probable).

DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly
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nilarity 88.2%;
Conservative
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is copyright. It is produced stitute of Bioinformatics and
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(La ribonucleoprotein
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RNA-BINDING (RRM).
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01-AUG-1992
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15-MAR-2004
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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PROSITE; PS00030; RRM_RNP 1; FALSE_NEG.

PROSITE; PS00030; RRM_RNP 1; FALSE_NEG.

RNA-binding; Nuclear protein; Phosphorylation.

RNA-BINDING (RRM).

DOMAIN 315 331

NUCLEAR LOCALIZATION SIGNAL

DOMAIN 315 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
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                                                                                                                                                                                                     J. Mol. Biol.
                                                                                                                                                                                                                        expression.";
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; (
Amphibia; Batrachia;
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                                                                                                                                                                                                                                                  Scherly D., Stutz
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                      "La proteins
                                                                                                                                                                                                                                                           MEDLINE=93287095;
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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                                                       PTM: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of La, LaA and LaB, in
SIMILARITY: HIGH, TO MAMPALLAN LA PROTEIN.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                               FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
DEVELOPMENTAL STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly constant steady state level in mature occytes, eggs, and early
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IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
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1. 23, Last
1. 43, Last
1 homolog A
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F., Lin-Marq N.,
Xenopus laevis.
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Chordata; Craniata; Vertebrata; Euteleostomi;
; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Systemic lupus erythematosus; RNI
Nuclear protein.
DOMAIN 111 187 RNA
MOD RES 366 366 PHO:
SEQUENCE 408 AA; 46837 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995
01-FEB-1995
28-FEB-2003
SMART; SHUUCALLES, PSS0102; RRM; L.

PROSITE; PSS01030; RRM RNP 1; 1.

PROSITE; PS00030; RRM RNP 1; 1.

RNA-binding; Nuclear protein; Phosphorylation.

RNA-binding; Nuclear protein; Phosphorylation.

RNA-BINDING (RRM).

47777 MW; 033FD9CC1E475F98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- 1
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection of species-specific variations.";
Gene 126:265-268(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=93246255; PubMed=7916708;
MEDLINE=93246255 H., Bartsch H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                          PIR; JC1494; JC1494.
InterPro; IPR002344; Lupus La.
InterPro; IPR006630; Lupus La_dom.
InterPro; IPR000504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSB OR SS-B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LA_RAT
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X67859; CAA48043.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                             Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.58, 58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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16; Conserv
                                                                                                                                                   ; PR00302; LUPUSLA.
SM00715; LA; 1.
SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AALEAQICQQIEYYFGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNAs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interacts with DDX15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 41, Last ar
homolog (La
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Last annotation update)
log (La ribonucleoprotein)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (BY CK2).
EC153C15F9187FC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-binding; Phosphorylation;
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1.2e-07;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
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                               CRC64;
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5S, 7S,
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RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary gland;

RX MEDLINE=22386257; PubMed=12477932;

RX MEDLINE=22386257; PubMed=12477932;

RX Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausner R.D., Collins F.S., Duetow K.H., Schaefer C.F., Bhat N.K.,

RA Altausner R.D., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Liausner R.D., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Jones S.J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J.M., Warra M.A.;

"Generation and mouse CDNA sequences ""

"The Collins of March Language Colli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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01-OCT-1993
15-MAR-2004
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P32067;
                                                                                                                                                                                                                                                                              Groelz D.,
Submitted (
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MEDLINE=93203630; PubMed=8454877;

MEDLINE=93203630; PubMed=8454877;

Topfer F., Gordon T., McCluskey J.;

"Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and reactivity of recombinant protein with poly(U) and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                        This
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                                                                                                                                           MILITED (OCT-1996) to the EMBL/GenBank/DDBJ databases.

FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7s, and 7-2 RNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunol. 150:3091-3100(1993).
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                                                              SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                              SUBUNIT: Interacts with DDX15
  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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(Rel.
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27,
43,
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Rodentia;
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(La ribonucleoprotein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87; DB 1;
Pred. No. 1.2e-07;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                       99:16899-16903 (2002)
                                                                                                            (By similarity) (Probable).
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                          a collaboration
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SEQUENCE OF 54-97 FROM N.A.

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RESULT 2
PRESENTATION OF THE PROPERTY O
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                                                                                                                                                    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Halesley A.W., Touchman J.W., Green E.D., Dickson M.C.,
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B., Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Matches
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p05455,
p05455,
p01-NOV-1988 (Rel. 09, Creact,
p1-NOV-1988 (Rel. 11, Last sequence update,
p1-NOV-1989 (Rel. 43, Last annotation update)
protein (Sjogren syndrome type B antigen) (SS-B)
protein (La autoantigen).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89202037; PubMed=2468131;
Chan B.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
sequences for RNA-binding.";
Nucleic Acids Res. 17:2233-2244(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                    Sturgess A.D., Coppel R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta, a MEDLINE=22388257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic structure and amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89053970; PubMed=3192525;
Chambers J.C., Kenan D., Martin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LA HUMAN
                                                                                   MEDLINE=88199081; PubMed
Sturgess A.D., Peterson
                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoantigen."
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                                               "Characteristics
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                 140:3212-3218(1988)
                                                                                                                           54-408
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                                                                                                        PubMed=2452201;
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Primates;
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acid sequence
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                                                                                   McNeilage L.J.,
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MIM; 109090; -. GO; GO: 00003729; GO: 0000049; GO: GO: 0008334; GO; GO: 0006400; I
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"The human La (SS-B) autoantigen interacts with putative DEAH-box RNA helicase.";
RNA 8:1428-1443 (2002).
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
SMOCSTTE: PS50102; RRM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04205; AAA51885.1; -
EMBL; BC001289; AAH01289.1;
EMBL; BC020818; AAH20818.1;
PIR; A31888; A31888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright: It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no rest
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"Function of the mammalian La protein: evide transcription termination by RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85166283; PubMed=3856888. Chambers J.C., Keene J.D.; "Isolation and analysis of cDNA of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:11316;
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                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELULAR LOCATION: Nuclear (Probable).

PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.

PTM: The N-terminus is blocked.

DISEASE: Sera from patients with systemic lupus erythemato often contain antibodies that react with the normal cellul La protein as if this antigen was foreign.

SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                 GO:0030529; C:ribonucleoprotein complex; TAS
GO:0003729; F:mRNA binding; TAS.
GO:0000049; F:tRNA binding; TAS.
GO:0008334; P:histone mRNA metabolism; TAS.
GO:0006400; P:tRNA modification; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and 7-2 RNAs.
SUBUNIT: Interacts with DDX15.
SUBCELLULAR LOCATION: Nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase III transcripts. It is associated of RNA polymerase III transcripts including
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                                                                                                                                                              PF00076;
                                                                                                                                                                                                   PF05383;
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                                                                                                                                                                                                                               IPR002344; Lupus_La.
IPR006630; Lupus_La_dom.
IPR000504; RNA_rec_mot.
                                                                                                                                                                  La; 1.
rrm; 1.
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igen on serine 366 can regul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evidence for erase III.";
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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8 xenopus lae
7 aedes albop
6 drosophila
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chlamydophi
canis famil
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ruta graveo
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ALIGNMENTS	YE14 SCHPO SEC6_RAT SEC6_HUMAN C4AA_BACTI CC11_CAEL TRPG_CAEL TRPB_NITEU LE3A_ASPNG VG41_BFT4 LBP_RABIT IFT4_HUMAN RPO2_COWPX
	O13869 schizosacch Q62825 rattus norv Q62825 rattus norv Q60645 homo sapien p16480 bacillus th p34641 caenorhabdi Q93971 caenorhabdi Q93972 nitrosomona p87256 aspergillus p04530 bacteriopha p17454 oryctolagus Q14879 homo sapien p17474 cowpox viru

N BOVIN D LA BOVIN D LA BOVIN D 1.01.11.1989 T 01.001.1989 T 28-FEB-2003 TISSUE-Pituitary; MEDLINE-89202037; PubMed-2468131; Chan E.K.L., Sullivan K.F., Tan E.M.; "Ribonucleoprotein SS-8/La belongs to a Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos. Lupus La protein homolog). EMBL; X13698; CAA31986.1; -. use the This + -- -NCBI_TaxID=9913; InterPro; IPR002344; Lupus La. InterPro; IPR006630; Lupus La_dom. InterPro; IPR00504; RNA_rec_mot. PIR; S03849; S03849. or send an email to license@isb-sib.ch). entities requires a modified between SEQUENCE FROM N.A. Bos taurus (Bovine). SUBUNIT: Interacts with DDX15 (By similarity). SUBCELLULAR LOCATION: Nuclear (Probable). FIM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN. SIMILARITY: Contains 1 RNA recognition motif (RRM) domain. s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial 7-2 RNAs. (Rel. 11, Created) (Rel. 11, Last sequence update) (Rel. 41, Last annotation update) otein homolog (La ribonucleoprotein) STANDARD; tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/ Cetartiodactyla; Ruminantia; Pecora; Bovoidea; PRT; 404 protein 8 family with (La autoantigen consensus forms 5S, 7S,

PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.

PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.

Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1.

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A;Molecule type: DNA
A;Residues: 1-166 <DAV>
A;Cross-references: EMBL:AF039051; PIDN:AAB94258.1; GSPDB:GN00023; CESP:C14C6.12
A;Experimental source: strain Bristol N2; clone C14C6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-529 <ROU>
A;Residues: 1-529 <ROU>
A;Cross-references: EMBL:ACC004005; NID:g3212846; PID:g3212854
A;Cross-references: EMBL:ACC004005; NID:g3212846; PID:g3212854
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
A; Xi, Kaul, S.; Rounsley, S.D.; Shea, T.D.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.D.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2943970 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F6E13.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00677; G84872
C;Accession: T00677; G84872
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
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T00677
Search completed: September 10, 2004, 18:02:25 Job time: 17.0782 secs
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A; Introns: 42/1; 156/3
                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                             A;Gene: F6E13.10; At2g43970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z14180
A;Accession: T00677
                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:g3212854; PIDN:AAC23405.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-529 <STO>
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Gene: CESP:C14C6.12
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61.5%;
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RNA-binding protein Lal homolog - fission yeast (Schizosaccharomyces N;Alternate names: La autoantigen; ribonucleoprotein La homolog C;Species: Schizosaccharomyces pombe
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Proc. Natl. Acad. Sci. U.S.A. 92, 5905-5909, 1995
A;Title: Modes of expression and common structural features
A;Reference number: Z18260; MUID:95320184; PMID:7597051
A;Recession: T14907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: the binding of the La protein to tRNA precursors is required for the C; Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                               A; Pathway: phenylpropanoid C; Superfamily: human cytoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, February 1998 A;Description: Screening of S. pombe cDNA library using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Utsumi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trans-cinnamate 4-monooxygenase C;Species: Petroselinum crispum
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Molecule type: mRNA
;Residues: 1-298 <UTS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000;Accession: T43542; T43325
                                                                                                                                                                                       Pathway: phenylpropanoid biosynthesis
;Superfamily: human cytochrome P450 CYP2D6; cytochrome
;Keywords: heme; iron; metalloprotein; oxidoreductase
;304-470/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated
                                                                                                                                                                                                                                                                        Description: catalyzes the formation of P-coumaric acid from trans-cinnamaric
                                                                                                                                                                                                                                                                                                              :Gene: C4H
                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-506 <LOG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 20-Sep-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene: sla1
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Residues: 1-298 <VAN>
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                                                                                                                                   Query Match
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7; Conserv
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                                                        AQICQQIEYYFGDF 18
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                                                                                                Conservative
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                                                                                                                                                                             iron (Cys)
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                                                                                                                  49.0%;
                        228
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                                                                                                4;
                                                                                                                  Score 47;
Pred. No.
                                                                                                                                                                         homology <P45>
s) (axial ligand)
                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
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Pred. No. 1.4
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                                                                                                                  DB 2;
5.4;
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                        A; Accession: T32701
                                                          R;David, M.; Wohldmann, P.; Bauer, submitted to the EMBL Data Library, A;Description: The sequence of C. e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              문
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A;Status: preliminary; translated
                                                                                                                  C; Accession:
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C; Accession: T30953
R; Sammons, L.; Wohl
hypothetical protein C14C6.12 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable RING zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: C44E4.4
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-396 < SAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, August 1999
A;Description: The sequence of C. elegans cosmid C44E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                               A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical protein A_IG002N01
                                                                                                                                                                                                                                                                                                        A;Gene: AT4g01270
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-506 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AF003140; PIDN:AAB54169.1
A;Experimental source: strain Bristol N2; clone C44E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
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                                                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Sequence and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402, 769-777,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; anonymous,
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Best Local
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8; Conserv
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                                                                                                                                                                        AQICQQIEYYFG 16
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Pred. No.
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Pred. No.
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17;
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Sprir

P.; Bauer, C.; Antoniou,

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29-Oct-1999 #text_change

29-Oct-1999

from GB/EMBL/DDBJ

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Mol. Cell. Biol. 14, 5123-5129, 1994
A;Title: Developmental characterization of a Drosophila RNA-binding protein homologous
A;Reference number: A53773; MUID:94309632; PMID:8035794
A;Accession: A53773
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J. Mol. 231, 196-204, 1993
A;Title: La proteins from Xenopus laevis. cDNA cloning and A;Reference number: S33817; MUID:93287095; PMID:8510143
A;Accession: S33818
A;Mclecule type: mRNA
A;Residues: 1-428 <SCH>
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A;Cross-references:
C;Genetics:
                                                                                                  Mol. Cell. Biol. 14, 5412-5424, 1994
A;Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae:
A;Reference number: A53781; MUID:94309661; PMID:8035818
A;Accession: A53781
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C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: leucine zipper; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    La/SS-B homolog D-la - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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                                       A; Molecule type: mRNA
A; Residues: 1-390 < YOO>
                                                                                                                                                                                     C;Accession: A53781
R;Yoo, C.J.; Wolin, S.L.
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Best Local S
Matches
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;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change
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Best Local S
                                                                              Status: preliminary
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151-158/Region: RNA-binding RNP1 motif
228-428/Domain: phosphorylated #status predicted <PHY>
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                   GB:L32988; NID:g488469; PID:g488470
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64.3%;
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Pred. No. 0.
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Pred. No. 0.57;
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: H89777
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H89777
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C;Superfamily: ribonucleoprotein La; ril
C;Keywords: RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Noticule type: DNA
A;Molecule type: DNA
A;Residues; 1-391 <KUR>
A;Cross-references: GB:BA000018; PID:g13700080; PIDN:BAB41379.1; GSPDB:GN00149
A;Cross-references: Strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                      rna binding protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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C;Superfamily: lipopolysaccharide biosynthesis protein bplD
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       capsular polysaccharide synthesis enzyme Cap5P [imported] - Staphylococcus aureus
                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-298 <BAD>
A;Cross-references: EMB
                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                A; Reference number: Z21818
A; Accession: T38937
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submitted to the EMBL Data
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                                                                                                                                               A; Introns: 72/1
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Matches
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                                    EAQICOOIEYYFGD
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2h-; cosmid c57A10
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Pred. No. 1.4;
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Pred. No. 1.3;
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Pred. No. 0.57;
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A; Introns:
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C; Keywords:
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A;Residues: 45-97,'LK' <CH3>
A;Residues: 45-97,'LK' <CH3>
A;Crose-references: GB:004205
A;Note: this sequence has been revised in reference A31888
R;Nyman, U; Ringertz, N.R.; Pettersson, I.
Immunol. Lett. 22, 65-72, 1989
A;Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
A;Reference number: A61051; MUID:89379261; PMID:2476379
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A;Residues: 'E',55-287,'V',289-408 <STU>
A;Residues: 'E',55-287,'V',289-408 <STU>
A;Crose-references: EMBL.M20328; NID:9337456; PIDN:AAA36577.1; PID:9337457
A;Cohsaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioka, K.
J. Clin. Invest. 85, 1566-1574, 1990
A;Title: Fine epitope mapping the human SS-B/La protein: Identification of a A;Reference number: I55553; MUID:90237237; PMID:1692037
A;Accession: I55553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA, A; Molecule type: mRNA, A; Residues: 1-19, E; Z1-47 < NYM>, R; Residues: 1-19, E; Z1-47 < NYM>, R; Rsturgess, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, J. Immunol. 140, 3212-3218, 1988
J. Immunol. 140, 3212-3218, 1988
J. Title: Characteristics and epitope mapping of a cloned human autoantigen I A; Reference number: S11013; MUID:88199081; PMID:2452201
A; Recession: S11013
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Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
A;Title: Isolation and analysis of cDMA clones expressing human lupus La antigen.
A;Reference number: A22956; MUID:85166283; PMID:3856888
A;Accession: A22956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 279-342 <R83>
A; Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
C; Comment: This protein associates with a variety of small RNA molecules,
ay act as a transcription termination factor.
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A;Residues: 81-107 <RES>
A;Cross-references: GB:M35261; NID:g338491;
A;Accession: I70205
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A; Residues: 1-408 < CH2>
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A;Status: translate
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A;Residues: 174-224 <RE2>
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                                                                                                                                                                                                                                                                                                                                                             Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2; Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology; Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                          ;112-178/Domain: ribonucleoprotein repeat homology <RRM>;113-118/Region: RNA.binding RNP2 motif
;135-158/Region: RNA.binding RNP1 motif
;228-408/Domain: phosphorylated #status experimental <PHY>
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                                                                                                                            Matches
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Pred. No.
28
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RESULT

ribonucleoprotein La.A - African clawed frog NyAlternate names: autoantigen SS-B/La; ribonucleoprotein SS-B. C;Species: Xenopus laevis (African clawed frog) C;Date: 03-Feb-1994 #sequence revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: S33818; S28545

S33818

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N,Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Xenopus laevis (African clawed frog) C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change C;Accession: S33817; S28544
R;Scherly, D; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: liver
C;Comment: This protein associates with a variety of small RNA molecules,
C;Comment: This protein associates with a variety of small RNA molecules,
ay act as a transcription termination factor.
C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: phosphoprotein; RNA binding
F;112-18/Domain: ribonucleoprotein repeat homology <RRM>
F;113-118/Region: RNA-binding RNP2 motif
F;151-158/Region: RNA-binding RNP1 motif
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A;Accession: JC1494
A;Molecule type: mRNA
A;Residues: 1-415 <SEM>
A;Cross-references: GB:X67859; NID:g55778; PIDN:CAA48043.1; PID:g55779
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                                                                                                                                                                                                                                                                            ay act as a transcription termination factor.

C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C;Keywords: phosphoprotein; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression A;Reference number: $33817; MUID:93287095; PMID:8510143 A;Accession: $33817
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A; Residues: 1-427 < SCH>
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227-427/Domain:
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Pred. No.
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Pred. No.
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96
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1: pir1:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 2 A31888 ribonucleoprotein La - human ribonucleoprotein S5-B/La; ribonucleoprotein S5-B; Sjogren syndrome antige C;Species: Homo sapiens (man) C;Date: 21-May-1990 #sequence revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: A31888; S03048; A22956; A61051; S11013; I55553; I70205; I70206; A31273 R;Ch:mbers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D. J. Bill. Chem. 263, 18043-18051, 1988 A;Title: Genomic structure and amino acid sequence domains of the human La autoantigen. A;Reference number: A31888; MUID:89053970; PMID:3192525 A;Accession: A31888 A;Molecule type: mRNA A;Residues: 1-408 <cha> A;Cross-references: GB:J04205; NID:9178686; PIDN:AAA51885.1; PID:9178687 A;Cross-references: GB:J04205; NID:9178686; PIDN:AAA51885.1; PID:9178687</cha>	Query Match 90.6%; Score 87; DB 1; Length 404; Best Local Similarity 88.9%; Pred. No. 6.7e-07; Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Oy 1 AALEAGICQUEYYFGDF 18	A;Residues: 1-404 <cha> A;Residues: 1-404 <cha> A;Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756 A;Note: part of this sequence was confirmed by protein sequencing C;Comment: This protein associates with a variety of small RNA molecules, most of which ay act as a transcription termination factor. C;Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology C;Keywords: blocked amino end; phosphoprotein; RNA binding F;112-178/Domain: ribonucleoprotein repeat homology <rmm> F;113-118/Region: RNA-binding RNP2 motif F;151-158/Region: RNA-binding RNP1 motif F;228-404/Domain: phosphorylated #status predicted <phy></phy></rmm></cha></cha>	RESULT 1 \$03849 ribonucleoprotein La - bovine N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B C;Species: Bos primigenius taurus (cattle) C;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999 C;Accession: \$03849 R;Chan, B.K.L.; Sullivan, K.F.; Tan, E.M. Nucleic Acids Res. 17, 2233-2244, 1989 A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences A;Reference number: \$03848; MUID:89202037; PMID:2468131 A;Accession: \$03849 A;Molecule type: mRNA

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      RESULT 1

LA BOVIN

ID LA B

AC P108

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SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
   PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
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Pfam; PF00076; rrm; 1.
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ALIGNMENTS	ATMA_SALTY MEI9_DROME	Y875_CHLTR	RBL_ECTSI	THIC_CLOPE	CYB_PARTE	ALKB_ARATH	Y818_PYRAE	IPYR_HAEIN	AGO1_ARATH	PLMN_MOUSE
	P36640 saimoneila Q24087 drosophila		P24313 ectocarpus							

Eukaryota; Metazoa; Cho Mammalia; Eutheria; Cet Bovidae; Bovinae; Bos. NCBI TaxID=9913; LA BOVIN P10881; EMBL; X13698; CAA31986.1; -. PIR; S03849; S03849. InterPro; IPR002444; Lupus_La_dom InterPro; IPR006630; Lupus_La_dom InterPro; IPR006504; RNA_rec_mot. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial MEDLINE-89202037; PubMed=24468131; Chan E.K.L., Sullivan K.F., Tan E.M.; Chan E.K.L., Sullivan K.F., Tan E.M.; Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding."; Nucleic Acids Res. 17:2233-2244(1989). -!- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7.2 PNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Lupus La protein homolog (La ribonucleoprotein) SSB. Bos taurus TISSUE=Pituitary; homolog). or send an email to license@isb-sib.ch). entities requires a license agreement (See http://www.isb-sib.ch/announce) -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain. SEQUENCE FROM N.A. SUBUNIT: Interacts with DDX15 (By similarity). SUBCELLULAR LOCATION: Nuclear (Probable). PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES C-TERMINAL PART OF THE PROTEIN. and 7-2 RNAs. (Bovine). STANDARD; Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; PRT; 404 B SITES ARE (La autoantigen Ą HH

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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chenration and initial analysis of more than 15,000 full-length
C. Maria M. Generation and mouse cDNA sequences.',
C. Maria M. Schmerch A., Schein J.E., Johnson M.S.,
C. Maria M. Schmerch A., Schals Sci. U.S.A. 99:16899-16903 (2002).
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01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Lupus La protein (Sjogren syndrome type B antigen) (SS-B)
ribonucleoprotein) (La autoantigen).
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Chan E.K.L., Sullivan K.F., Tan E.M.;
"Ribonucleoprotein SS-B/La belongs to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA-binding.";
Res. 17:2233-2244(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263:18043-18051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                       8 FROM N.A.
PubMed=2452201;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
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                                           epitope mapping of
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                                                                         3
                                                                         <u>ن</u>و:
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4EE30B5C262AD6A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Pred. No.
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                                                                       McNeilage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keene J.D.;
                                           a cloned human, autoantigen
                                                                       L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.1e-09;
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                                                                       Whittingham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family with
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GO; GO:0030529; C:ribonucleoprotein complex; GO; GO:0003729; F:mRNA binding; TAS. GO; GO:000049; F:tENA binding; TAS. GO; GO:0008334; P:histone mRNA metabolism; TAG. GO; GO:0006400; P:tENA modification; TAS.
                                                                                                                                                                                                   MIM;
                                                                                                                                                                                                                                          EMBL; X13697; CAA31985.1; -.
EMBL; J04205; AAA51885.1; -.
EMBL; BC001289; AAH01289.1; -.
EMBL; BC020818; AAH20818.1; -.
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97207017; PubMed=9054510; Fan H., Sakulich A.L., Goodier J.L., Zhang X., "Phosphorylation of the human La antigen on se recycling of RNA polymerase III transcription Coll 88:707-715(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gottlieb E., Steitz J.A.; "Function of the mammalian Latranscription termination by
                         PRINTS; PR00302; LUPUS SMART; SM00715; LA; 1.
                                                       Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
                                                                                                                                                                                                                              EMBL; BC020818; AAH2
FIR; A31888; A31888.
                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative DEAH-box RNA helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fouraux M.A., Kolkman M.J.M., Van
Van Venrooij W.J., Pruijn G.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chambers J.C., Keene J.D.; "Isolation and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 54-97 FROM N.A. MEDLINE=85166283; PubMed=3856888;
                                                                                    InterPro;
                                                                                                InterPro; IPR006630;
                                                                                                             InterPro; IPR002344; Lupus_La.
                                                                                                                                                                                                                  Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22346609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH DDX15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and 7-2 R
SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 often contain antibodies that react with the normal cellul
La protein as if this antigen was foreign.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Probable).

FIM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES A
C-TERMINAL PART OF THE PROTEIN.

FIM: The N-terminus is blocked.

DISEASE: Sera from patients with systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.55, 55, 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8:1428-1443 (2002) .
                                                                                                                                                                                                   109090;
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                                                                                                                                                                                                                HGNC:11316; SSB.
               SM00360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7-2 RNAs.
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                                                                                    IPR000504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acad. Sci. U.S.A. 82:2115-2119(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interacts with DDX15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SS-B) autoantigen interacts with DDX15/hPrp43,
                                          LUPUSLA
RRM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=12458796;
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                                                                            Lupus_La_dom; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              der Heijden A.,
                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressing human
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on serine
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366 can
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                                                                                                                                                                                                                                                                                                                                                                                             a collaboration -
MBL outstation -
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RESULT 3
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PAC 14
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01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LA RAT
P38656;
SMART; SHOULD KKE, 1.
SMART; SMOULD KKE, 1.
PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Systemic lupus erythematosus; RNA-binding; Phosphorylation; Nuclear protein.

DOMAIN 111 187 RNA-BINDING (RRM).

MOD_RES 366 PHOSPHORYLATION (BY CK2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of rat cDNA clones coding for the autoantigen SS-B/La: detection of species-specific variations.";

Gene 126:265-268(1993).
-!- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.58, 58, 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                   PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                  Pfam; PF05383; La; 1. Pfam; PF00076; rrm; 1
                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X67859; CAA48043.1; PIR; JC1494; JC1494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                              InterPro; IPR002344;
InterPro; IPR006630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93246255; PubMed=7916708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSB OR
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                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7-2 RNAs.
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                                                                                                                                                                                                                                                                                                     IPR000504;
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408 AA;
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(Rel. 31, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46837 MW;
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                                                                                                                                                                                                                                                                                                     RNA_rec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (La ribonucleoprotein) (La autoantigen
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; EC153C15F9187FC4 CRC64;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT AND TO THE SULT AND THE 
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SEQUENCE FROM N.A.

SERAIN FVB/N; TISSUE=Mammary gland;

STRAIN FVB/N; TISSUE-Mammary gland;

STRAIN FVB/N; TISSUE-MAMMARMARY MARY M.A.;

STRAIN FVB/N; TISSUE-MAMMARY MARY M.A.;

STRAIN FVB/N; TISSUE-MAMMARY MARY M.A.;

STRAIN FVB/N; TISSUE-MAMMARY MARY M.A.;

STRAIN FVB/N; TISSUE-MAMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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MEDLINE-93203630; PubMed-8454877;
MEDLINE-93203630; PubMed-8454877;
Topfer F., Gordon T., McCluskey J.;
"Characterization of the mouse autoantigen La (SS-B). Id of conserved RNA-binding motifs, a putative ATP binding of conserved RNA-binding motifs, a putative ATP binding motifs, a putative ATP binding motifs, a putative ATP binding of conserved RNA-binding motifs, a putative ATP binding motifs, a putative ATP binding of conserved RNA-binding motifs, a putative ATP binding motifs, a putative ATP binding
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P32067;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-11 FROM N.A.

Groelz D., Bachmann M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Generation and initial analysis of more than human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                      and 7-2 RNAs.
SUBUNIT: Interacts with DDX15 (By similarity).
SUBCELLULAR LOCATION: Nuclear (Probable).
PTM: Phosphorylated (By similarity).
SIMILARITY: Contains 1 RNA recognition motif (
                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor form of RNA polymerase III transcripts including tRNA and 4.58, 58, 7
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                                                                                                                                                Contains 1 RNA recognition motif (RRM) domain.
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Pred. No. 3.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99:16899-16903 (2002)
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5S, 7S,
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Best Local (
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GO; GO:0005634; C:nucleus; IDA.
InterPro; IPR002344; Lupus La.
InterPro; IPR006530; Lupus La.
dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00376; rrm; 1.
PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P28049;
01-AUG-1992 (Rel. 2
01-AUG-1992 (Rel. 2
15-MAR-2004 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00360, ....., PROSITE; PS50102; RRM; 1.
PROSITE; PS501030; RRM; RNP 1; 1.
PROSITE; PS00030; RRM RNP 1; 1.
RNA-binding; Nuclear protein; Phosphorylation.
RNA-binding; Nuclear RNA-BINDING (RRM).
111 187 RNA-BINDING (RRM).
47756 MW; 2D75197692FDC933 CRC64;
                                                                                                                                                                      expression.";
J. Mol. Biol. 231:196-204(1993).

J. Mol. Biol. 231:196-204(1993).

-:- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts (By similarity).

-:- SUBCELULAR LOCATION: Nuclear (Probable).

-:- DEVELOPMENTAL STAGE: Barely detectable in stage I/I occytes,
accumulate in stage III/IV occytes, then exhibit a roughly
constant steady state level in mature occytes, eggs, and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L00993; AAA39415.1; -. EMBL; BC003820; AAH03820.1; EMBL; Y07951; CAA69249.1; -.
                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93287095;
Scherly D., Stutz
"La proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Oocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
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                                                                PTW: Phosphorylated (Probable).
MISCELLANEOUS: There are two forms of La, LaA and LaB, in SIMILARITY: HIGH, TO MANMALIAN LA PROTEIN.
SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XENLA
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SWISS-PROT entry is copyright. It is produced through a collaboration -
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1 homolog B
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43,
                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8510143;
F., Lin-Marq N.,
Xenopus laevis.
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100.0%;
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annotation update)
(La ribonucleoprotein
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   and developmental
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; Pipidae;
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RESULT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992
01-AUG-1992
15-MAR-2004
                                                                                                                                                                                                                                                                              "La proteins from Xenopus laevis. CDNA cloning and developmental expression.";
J. Mol. Biol. 231:196-204(1993).
i. FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts (By similarity).
polymerase III transcripts (By similarity).
i. SUBCELLULAR LOCATION: Nuclear (Probable).
i. SUBCELLULAR STAGE: Barely detectable in stage I/II occytes, accumulate in stage III/IV occytes, then exhibit a roughly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAA_XENLA
P28048;
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PROSITE; P800030; RRM RNP 1; FALSE NEG.
RNA-binding; Nuclear protein; Phosphorylation.
DOMAIN 10 202
RNA-BINDING (RRM)
DOMAIN 315 331 NUCLEAR LOCALIZAT
DOMAIN 315 331 NUCLEAR LOCALIZAT
                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002344; Lupus_La.
InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF05383; La; 1.
Pfam; PF00076; rrm; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00302; LUPUSLA.
SMART; SM00715; LA; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93287095;
Scherly D., Stutz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
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                                                                                                                    embryos.

PTM: Phosphorylated (Probable).

PTM: Phosphorylated (Probable).

MISCELLANEOUS: There are two forms of La, LaA and LaB, in:

SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.

SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
                                                                                                                                                                                                                                                              constant
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315
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ilarity 80.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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l. 23, Last s
l. 43, Last a
n homolog A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=8510143; F., Lin-Marq N.,
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annotation update)
(La ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a; Craniata; Vertebrata; Euteleostomi;
Mesobatrachia; Pipoidea; Pipidae;
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Pred. No. 0.00027;
1; Mismatches 2;
                                                                                                                                                                                                                                                              in mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clarkson S.G.;
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Best Local S
Matches 11
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PRINTS; PROGOZO; LUPUSLA.

SMART; SM00715; LA; 1.

SMART; SM00360; RRM; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRM; 1.; 1.

PROSITE; PS00030; RRM RNP_1; 1.

PROSITE;
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28-FEB-2003 (Rel. 41, Last sequence update)
La protein homolog (La ribonucleoprotein) (La autoa Aedes albopictus (Forest day mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Nematocera; Culic NCBI TaxID=7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q26457;
15-JUL-1998
15-JUL-1998
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X68817; CAA48
PIR; S33818; S33818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR006630; Lupus_La_dom.
InterPro; IPR000504; RNA_rec_mot.
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Pfam; PF00076; rrm; 1
                                                                    InterPro; IPR002344;
InterPro; IPR006630;
InterPro; IPR000504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL S
MEDLINE=96135233; PubMed=8551578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LA AEDAL
  PRINTS; PR00302; LUPUSLA
                                                                                                              InterPro;
                                                                                                                                        EMBL; S80954; AAB35931.1;
                                                                                                                                                                                                                                                                                                                                                            amounts are present in the cytoplasm. SIMILARITY: Contains 1 RNA recognition motif SIMILARITY: TO VERTEBRATE PROTEIN LA.
                         PF05383; La; 1. PF00076; rrm; 1
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                                                               Lupus_La_dom.
RNA_rec_mot.
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78.6%;
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Pred. No. 0.00
1; Mismatches
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RNA-BINDING (RRW).

NUCLEAR LOCALIZATION SIGNAL

NUCLEAR LOCALIZATION SIGNAL

NUCLEAR LOCALIZATION SIGNAL

SEBJA38B7D2E3EC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                            ght. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                      (RRM)
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan R.P., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Posler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Wei M.-H., Ibsgwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibsgwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Best Local S
Matches 10
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SMART; SM00360; RRM; 1.
PROSITE; PS00102; RRM; 1.
PROSITE; PS00030; RRM RNP 1; FALSE NEG.
RNA-binding; Nuclear protein; DNA-binding.
RNA-BINDING (
RNA-BINDING (
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"Developmental characterization of a Dr
homologous to the human systemic lupus
La/SS-B autoantigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Canton-S; TISSUE-Ovary;
MEDIJINE-94309632; PubMed-8038794;
Bai C., Li Z., Tolias P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LA DROME STANDARD; PRT; 390 AA. P40795; Q24375; Q29VIN2; Q1-FEB-1995 (Rel. 31, Created) 16-DCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) La protein homolog (La ribonucleoprotein) (La LA OR CG10922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "La proteins from Di
cerevisiae: a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ephydroidea; Dro
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yoo C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94309661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wolin S.L.;
iins from Drosophila melanogaster and Saccharomyces
io: a veast homolog of the La autoantigen is dispensable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. 14:5412-5424(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8035818;
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Pred. No. 0.085;
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RA Liu X., Mattei B., McIntosh T.C., McIscod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Mcris J., McSheri A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Molson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Fertor C., Par S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun S.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.",
"In genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
"C. jolymerase III transcripts. May play a specialized role during fly
"C. development."
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                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                             FlyBase; FBgn0011638; La.

GO; GO:0008098; F:SS rRNA primary tra
GO; GO:0003723; F:RNA binding; NAS.

InterPro; IPR002344; Lupus La.

InterPro; IPR002347; Lupus La.

InterPro; IPR006630; Lupus La.

InterPro; IPR006630; Lupus La.

Ffam; PF00363; La; 1.

Pfam; PF00376; rrm; 1.

Pfam; PF00076; rrm; 1.

PRINTS; PR00302; LUPUSLA.

SMART; SM00300; RRM; 1.

SMART; SM00300; RRM; 1.

PROSITE; PS00030; RRM; 1.

PROSITE; PS000300; RRM; 1.
                                                                                                                                         CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U07652; AAA20518.1; -.
EMBL; L32988; AAA21776.1; -.
EMBL; AE003666; AAF53885.1; -.
PIR; A53773; A53773.
PIR; A537781; A53781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See l or send an email to license@isb-sib.ch).
                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                       RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glands.
SIMILARITY: Contains 1 RNA recognition motif SIMILARITY: TO VERTEBRATE PROTEIN LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STACE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo followed by a restricted pattern of mesodermal expression that later confined to the visceral mesoderm, gonads, gut, and saliv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
51
                             Α
                                                             similarity
9; Conser
                                                                                                                                                                                                   PS50102; RRM; 1.
PS00030; RRM RNP 1; 1.
ing; Nuclear protein; D
149 234 RN
                             EAKICHQIEYYFGD
                                                                                                                        390
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182
283
329
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                                                             Conservative
                                                                                                                        ΑA;
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183
                                                                                                                          44884
                                                                          51.5%;
64
                                                                                                                          MW;
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Pred. No.
                                                    Pred. No. v. ...
1; Mismatches
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- ' '
                                                                                                                                                                       A -> T (IN REF. 1).

KH -> NS (IN REF. 1).
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RNA-BINDING (RRM)
                                                                                                                          A8099288B90446A5
                                                                                                                                         R (IN REF. 1).
N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                transcript binding; IDA
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(See http://www.isb-sib.
                                                                            0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rmatics and the EMBL outst
                                                                                         DB 1; Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
                                                                                                                            CRC64;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain.
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RESULT
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown S., Chillingworth T., Churcher C.M.,
RA Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Goney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA RA Chiler S., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Waltjens I., Vonstreels E., Rieger M., Schaefer M., Whitehead S.,
RA Waltjens I., Vanstreels E., Rieger M., Schaefer M., Wheller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Ger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
"The genome sequence of Schizosaccharomyces pombe.";
RI Nature 415:871-880 (2002). Barrell B.G., Nurse P.;

"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=98067398; PubMed=9404894;

van Horn D.J., Yoo C.J., Xue D., Shi H., Wolin S.L.;

"The La protein in Schizosaccharomyces pombe: a conserved yet dispensable phosphoprotein that functions in tRNA maturation.";

RNA 3:1434-1443(1997).
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P87058; 013
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
La protein homolog (La ribonucleoprotein) (
SLAI OR SPAC57A10.10C.
EMBL; AF022949; AAB82145.1; -. EMBL; AB011371; BAA24981.1; -. EMBL; Z94864; CAB08173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Binds to the precursors of polymerase Functions in tRNA maturation. SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 RNA recognition motif SIMILARITY: TO VERTEBRATE PROTEIN LA.
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                                                                                                                                                                                                                                                                                                                    restrictions
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RESULT
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CONFLICT
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SMART; SM00715; LA; 1.
SMART; SM00306); RRM; 1.
PROSITE; PSS0102; RRM; 1.
PROSITE; PS00030; RRM RNP_1; FALSE_NEG.
RNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05383; La; 1
Pfam; PF00076; rrm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GeneDB_SPombe;
This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                            Nucleic Acids Res. 31:2134-2147(2003).

-I- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases. The reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q823W6;
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHLCV
                                                                                                                                                                                                                                                                                                                                                Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., Wi
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC 6.3.5.-) (Asj
GATB OR CCA00289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Aspartyl/glutamyl-tNNA(Asn/Gln) amidotransferase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; T43542; T43542.
                                                                                                                                                                                                                                                                                               examining the role of niche-specific Chlamydiaceae.";
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InterPro; IPR000504;
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                                                                                                                                                                                                                                                                                                                           "Genome sequence of Chlamydophila caviae
                                                                                                                                                                                                                                                                                                                                       Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22569155; PubMed=12682364;
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-GPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=83557;
                                                                                                                                                                                         similarity)
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IPR006630; Lupus_La.
IPR000504; RNA_rec_n
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298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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M -> I (IN REF. 1 AND 2).
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1 N.B., Cart
                                                                                                                                                                                                                                                                                                                                                                     White
                                                                                                                                                                                                                                                                                                                                                       Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                Carty H.A.
                                                                                  a collaboration
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RESULT
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Best Local S
Matches
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TCMO PETCR STANDARD;

15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic Trans-cinnamate (CA4H) (C4H) (P450C4H) (Cytochrome P450 73)
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudiootyledons; core eudicots; aster. campanulids; Apiales; Apiaceae; Apioideae; apioid superclade; Apium clade; Petroselinum.
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Protein biosynthesis; Ligase; Complete proteome.
SECULENCE 487 AA; 54571 MW; 7D4E0EE7760A0AF7
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Pfam; PF02934; GatB N; 1.
Pfam; PF02637; GatB Yeey; 1.
TIGRPAMS; TIGR00133; gatB; 1.
PROSITE; PS01234; GATB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
InterPro;
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TIGR; CCA00289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Modes of expression and common structural features of the cuphenylalanine ammonia-lyase gene family in parsley.";

Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995)

-I- FUNCTION: Controls carbon flux to pigments essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00121; -; 1.
                                                                                                                                                                 EMBL; L38898; AAC41660.1; PIR; T14907; T14907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95320184; PubMed=7597051;
Logemann E., Parniske M., Hahlbrock K.;
                                                                                                           InterPro; IPR001128;
Pfam; PF00067; p450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pollination or UV protection, to numerous pytoalexins synthesized
by plants when challenged by pathogens, and to lignins
CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydroxycinnamate + NADP(+) + H(2)O. PATHWAY: Lignin biosynthesis. PATHWAY: Phenylpropanoid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228
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; IPR006107; GatB_cent.
; IPR006075; GatB_N.
; IPR003695; GatB_Yqey.
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Pred. No.
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12;
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PRINTS; PR00385; P450 PROSITE; PS00086; CYTO Oxidoreductase; Monoo

Monooxygenase

Heme;

NADP

IRON (HEME AXIAL LIGAND)

(BY SIMILARITY).

CYTOCHROME_P450; 1.

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RESULT 12
GLNO_BACST
ID GLNO_BACST
AC P27675;
DT 01-AUG-1992
                                        RESULT 13
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NP BIND
SEQUENCE
LBP_RABIT
P17454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; irnver: 1.

Pfam; PF00005; ABC tran; 1.

ProDom; PD000006; ABC transporter;

ProDom; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M61017; AAA22483.1; -.
PIR; A42478; A42478.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu L., Welker N.E.;
"Cloning and characterization of a glutamine transport operon of Bacillus stearothermophilus NUB36: effect of temperature on regulation of transcription,";
J. Bacteriol. 173:4877-4888(1991).
J. Bacteriol. 173:4877-4888(1991).
J. Bacteriol. 173:4877-4888(1991).
J. Bacteriol. 173:4877 OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR GLUTTAMINE. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1
Amino-acid transport; Transport; Membrane; ATP-binding.
NP_BIND 34 41 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Bacil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glutamine transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSPORT SYSTEM.
SUBCELLULAR LOCATION: Membrane-associated (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the ABC transporter family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _TaxID=1422;
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                                                                                                                                                                                                                                                           Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRLAQSFEYHFGDF 228
                                                                                                                                                                                                           HQIEYYFGDF 18
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                                                                                                                                                                                                                                                                                                                                                                  242 AA;
                                                                                                                                                                                                                                                              Conservative
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23, Last sequence update)
40, Last annotation update)
rt ATP-binding protein glnQ.
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                                                                                                                                                                                                                                                                                                                                                                  27436 MW;
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                                                                                                                                                                                                                                                           Score 42; DB Pred. No. 8.4; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB
Pred. No. 12;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillaceae;
                           482
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                                                                                                                                                                                                                                                                                                               Length 242;
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                                                                                                                                                                                                                                                                                                                                                                  CRC64;
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RESULT 14
FOL2 MOUSE
ID FOL2 MOUSE STANDARD;
AC Q05685;
DT 01-JUN-1994 (Rel. 29, Created)
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                           Pfam; PF01273; LBP_BPI_CETP.
Pfam; PF02886; LBP_BPI_CETP_C; 1.
SMART; SM00328; BBPI; T.
SMART; SM00328; BBPI; 1.
SMART; SM00329; BBPI; 1.
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86306528; PubMed=2427635;
Tobias P.S., Soldau K., Ulevitch R.J.;
"Isolation of a lipopolysaccharide-binding acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=90385281; PubMed=2402637; Schumann R.R., Leong S.R., Flaggs G.W., Gray P.W., Wright S.D., Mathison J.C., Tobias P.S., Ulevitch R.J.; Mathison J.C., Tobias P.S., Ulevitch R.J.; "Structure and function of lipopolysaccharide binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Lipopolysaccharide-binding protein precursor
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35534; AAA99235.1; -. PIR; B35843; B35843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rabbit serum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 249:1429-1431(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P17213; 1BP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 27-66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Binds to the lipid a moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in membrane of all Gram-negative bacteria. The LBP/LPS to interact with the CD14 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family.
                                                                                             194
                                                                                                                                                                                                                                                                                                               transport;
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8; Conser
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                                                                                                                     LEAKICHQIE
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PS00400; LBP BPI CETP; 1.
PROPERTY Antibiotic; Transmembrane; Glycoprotein; Signal
                                                                                             LESKICRQIE
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301
351
387
                                                                                                                                                   Conservative
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482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license
                                                                                                                                                            42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agreement
                                                                                                                                                                                                                LIPOPOLYSACCHARIDE-BINDING PROTEIN.
N-LINKED (GLCUAC. ) (POTENTIAL).
N-LINKED (GLCUAC. . ) (POTENTIAL).
N-LINKED (GLCUAC. . ) (POTENTIAL).
E -> G (IN REF. 2).
S -> F (IN REF. 2).
                                                                                                                                                                 Score 42; DB
Pred. No. 17;
                                                                                                                                                                                                        628A6E0A647200C2 CRC64;
                                                                                                                                                   Mismatches
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                             251
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                             AA.
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RESULT 15

IFT4_HUMAN STANDARD;

ID TFT4_HUMAN STANDARD;

AC 014879; Q99634; Q9BSK7;

DT 30-MAY-2000 (Rel. 39, Crea

DT 30-MAY-2000 (Rel. 39, Last

DT 10-OCT-2003 (Rel. 42, Last
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Best Local S
Matches 6
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-94140851; PubMed=8307991;
Brigle K.E., Seither R.L., Westin E.H., Goldman I.D.;
Brigle K.E., Seither R.L., Westin E.H., Goldman I.D.;
"Increased expression and genomic organization of a folate-binding protein homologous to the human placental isoform in L1210 murine leukemia cell lines with a defective reduced folate carrier.";
J. Biol. Chem. 269:4267-4272(1994).
J. Biol. Chem. 269:4267-4272(1994).

-i-FUNCTION: Binds to folate and reduced folic acid derivatives and mediates delivery of 5-methyltetrahydrofolate to the interior of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
PROPEP
LIPID
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J. Biol Char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brigle K.E., Westin E.H., Houghton M.T., Goldman I.D.; "Characterization of two cDNAs encoding folate-binding L1210 murine leukemia cells. Increased expression associated the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=91373339; PubMed=1894617;
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10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M64817; AAA37599.1; -. EMBL; L25338; AAA37594.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-49 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004269; Folt_chemrecept.
Pfam; PF03024; Folate_rec; 1.
Receptor; Glycoprotein; Signal; Placenta; Folate-binding; Membrane;
GPI-anchor; Multigene family; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells.
SUBCELLULAR LOCATION: Attached
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                 Similarity
6; Conserv
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228
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(Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                     Conservative
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to the
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                                                                                                                                                                                                                                                                                                     Score 41; DB Pred. No. 13; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
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GPI-anchor amidated serine
N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein.
POTENTIAL.
FOLATE RECEPTOR BETA.
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                8404EACEB1BFECC7 CRC64;
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                                                                                               490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                   Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for commercial ib.ch/announce/
                                                                                                                                                                                                                                                                                                        0
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DE BREER PROCECCE CONTRARE REPRESE REP
                EMBL; AFV...

EMBL; AF083470; A4V...

( EMBL; U52513; AAB40606.1; -..

R EMBL; BC001383; AAH01383.1; -..

EMBL; BC004977; AAH04977.1; -..

"CNC:5411; IFIT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Halkerly, B.W. The Martin M. M. Schernen M. Frankers M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- SIMILARITY: Belongs to the IFIT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-98054347; PubMed-9391139;
Zhu H., Cong J.P., Shenk T.;
"Use of differential display analysis to assess the effect cytomegalovirus infection on the accumulation of cellular Finduction of interferon-responsive RNAs.";
Proc. Natl. Acad. Sci. U.S.A. 94:13985-13990(1997).
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu M., Tong J., Mao M., Chen S., Chen Z.;
"RIG-G, a novel gene induced by ATRA in acute promyelocytic leukemia cells, is a new member of the ISG family.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=99047533; PubMed=9828129; de Veer M.J., Sim H., Whisstock J.C. "IF160/ISG60/IF1T4, a new member of interferon-stimulated genes."; genomics 54:267-277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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|Retinoic acid-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterferon-induced
                                                                                                                                                                                AF026939; AAB95160.1; -. AF083470; AAC63524.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid-induced
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d 60 kDa protein) (IFI-60K) (ISG-60) (CIG49)
uced gene G protein) (RIG-G).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
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he human IFI54/IFIT2 family
                                                                                                                                                                                                                                                                                                          noved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.E.,
                                                                                                                                                                                                                                                                                                                          is
is
                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
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DR InterPro; IPR001440; TPR.

DR SMART; SM00028; TPR; 4.

EXEMITY SM00008; TPR; 4.

EXEMITY SM000028; TPR; 4.

EXEMITY SM000028; TPR; 4.

EXEMITY SM00008; TPR; 4.

EXAMPTITY SM00008; TPR; 4.

EXEMITY SM00008; TPR; 4.

EXAMPTITY SM00008; TPR; 4.

EXAMPTIT
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RESULT 14 US-10-054-611-26

Sequence 26, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:

Cech, Thomas R.

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RESULT 15
US-10-170-385-477
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Sequence 477, Application US/10170385
Publication No. US20030203372A1
GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert
                                                                                                                                                                                                                                                                                                            Query Match 67.9%;
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION UNMBER: 08/854,050

FILING DATE: <Unknown
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: APPLE, Randolph T.

REGERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030059787A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: No. US20030059787A1 Relevant
TOPOLOGY: No. US20030059787A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300
RMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PATENTIN: PC-DOS/MS-DOS

SOFTMARE: PATENTIN: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/054,611

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                      1 ILROVEYYFGD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                    Score 57; DB 14; Length 39; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                 ٥,
                                                                                                                                                                                                                                                                                                                 Indels
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APPLICANT: Krige, David
FITTLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 477
LENGTH: 408
TYPE: PRT
ORGANISM: Homo Sapiens
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                                                                                                                                                       US-10-170-385-477
                                                                        Best Local Similarity Matches 10; Conserv
                                                                                                               Query Match
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APPLICANT:
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14 EAKICHQIEYYFGDF 28
                                    2 ERAIIRQVEYYFGDF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kingsman, Susan Mary
                                                                    67.9%; Score 57; DB 1
ilarity 66.7%; Pred. No. 0.25;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert Alan
                                                                                                               DB 12; Length 408;
                                                                            Indels
                                                                              0
                                                                              Gaps
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Search completed: September 10, 2004, 18:11:58 Job time : 36.9436 secs

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TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-325-810-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-053-758-26; Sequence 26, Application US/10053758; Publication No. US20030032075A1
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; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SUS-10-053-758-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Cech
                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 67.9%;
Local Similarity 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
TITLE OF INVENTION: No. US20030032075Alel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER; 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                          ATTORNEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/053,758 FILING DATE: 18-Jan-2002 CLASSIFICATION: 536
                                              TYPE; amino acid
STRANDEDNESS: NO. US20030032075A1 Relevant
TOPOLOGY: NO. US20030032075A1 Relevant
PULE TYPE: peptide
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                                                                                                                                                                                          TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
NEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-APR-1997
                                                                                                                               ENGTH: 39 amino acids
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                          SEQ ID NO: 26:
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Pred. No. 0.021;
1; Mismatches
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                                                                                                          US-10-054-295-26
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Publication No. US2003
GENERAL INFORMATION:
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                                     Matches
                                                        Best
                                                                      Query Match
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/854,050
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
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                                                        Local
                                                                                                                             STRANDEDNESS: NO. US20030044953A1 Relevant TOPOLOGY: NO. US20030044953A1 Relevant MOLECULE TYDE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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TITLE OF INVENTION: No. US20030044953Alel Telomerase
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                                                                                                                                                                                                  LENGTH: 39 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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vo. US20030044953A1
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                                       Conservative
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Chapman, Karen B.
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                                                        67.9%;
90.9%;
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Pred. No. 0.021;
                                     Score 57; DB 14; Length 39; Pred. No. 0.021; indels
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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-766-253-26
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Matches
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Best Local Similarity
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                                                                                                                                            TELEFAX: (415) 576-0300
NFORMATION FOR SEQ ID NO: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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FITLE OF INVENTION: No. US20030009019A1el Telomerase
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COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                     LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not rele
                                                                                                                                                                                                                                                                NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
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Two Embarcadero Center, 8th Floor
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Nakamu
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Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
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not relevant
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Pred. No.
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Best Local Similarity
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                           TELEFAX: (415) 576-03: INFORMATION FOR SEQ ID NO: 216: SEQUENCE CHARACTERISTICS:
                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                                                                                                 NAME: Ausenhus, Scott L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                            PLICATION NUMBER:
VILING DATE: 14-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LING DATE: 01-OCT-1996
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                        APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/325,810 FILING DATE: 20-Dec-2002
                                                                        REGISTRATION NUMBER: 42,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/402,181 FILING DATE: 29-Sep-1997 APPLICATION NUMBER: US 08/724,643
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                     APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                  PPLICATION NUMBER: US 08/854,050
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TLING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ICATION NUMBER: US 08/851,843
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                                                                                                                                                                                                                                                                                US 08/912,951
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                                                  015389-002620US
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Query Match
Best Local Similarity
Matches 10; Conserve
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Sequence 26, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Bovine US-09-836-073-14
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SEQ ID NO 14
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
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TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18
                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrews, William H.
TITLE OF INVENTION: No. US20020164786A1el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
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ATTORNEY/AGENT INFORMATION
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                    FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                          FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                           APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/846,017
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                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
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Chapman, Karen B.
Morin, Gregg B.
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Pred. No. 0
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US-09-766-253-26
; Sequence 26, App
; Publication No.
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                                                                                          INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                      APPLICATION NUMBER: US 08/724,643

PILING DATE: 01-0CT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrews, William H.
TITLE OF INVENTION: No. US20020187471A1el Telomerase
NUMBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
      STRANDEDNESS: not rele
TOPOLOGY: not relevant
                                                                                                                                    TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
                                               TYPE: amino acid
                                                                     LENGTH: 39 amino acids
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not relevant

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INFORMATION FOR SEQ ID NO: 26:
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LENGTH: 39 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20020164786A1 Relevant
TOPOLOGY: No. US20020164786A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION:
                                                                           APPLICANT: Cech, Thomas R
                                                                                                                                                                                                                           1 ILRQVEYYFGD 11
                                                                                                                                                                                                                                                              5 IIRQVEYYFGD 15
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Similarity 90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randol REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415)
                                                                                                                              Application US/09766253
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                US20020187471A1
               Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                      ingner, Joachim
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NUMBER: 36,429
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APPLICANT: Dasyupts, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-2
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; ORGANISM: Homo Sapiens
US-09-836-073-4
                                                                                                                                                                                                                                                                                                                                 RESULT 4
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application us
Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          Sequence 13, Application US/09836073
Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dasgupta, Asim APPLICANT: Das, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18
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66.7%;
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Pred. No. 0.0013;
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; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13
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US-09-836-073-1
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                                                                                                                               US-09-836-073-5
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APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
CURRENT FILING DATE: 2002-10-24
                                                              Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                               SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09836073 Patent No. US20020173475A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09836073 Patent No. US20020173475A1
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
CURRENT FILING DATE: 2002-10-24
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/316,630 PRIOR FILING DATE: 1999-05-21 NUMBER OF SEQ ID NOS: 19
                                                                                                                                           LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                        1 QERAIIRQVEYYFGDF 16
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Pred. No.
                                                                           Score 57; DB 9;
Pred. No. 0.0095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 9;
Pred. No. 0.0089;
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                                                               Mismatches
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0.0095;
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                                                               Gaps
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
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seq length: 2000000000
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Published Applications AA:*

1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2 6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

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143.151 Million cell updates/sec
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Gapop 10.0 , Gapext 0
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Listing first 45 su
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	10 12	989	Φ υ Φ	ω N P	Result No.
57 57	577	57 57	57 57 57	562 582	Score
67.9	67.9 67.9	67.9 67.9	67.9 67.9 67.9	100.0 73.8 69.0	Query Match L
39 408		3998	17 18 18	16 18	Length I
14 12	12	999	999	ဖဖဖ	BB
US-10-054-611-26 US-10-170-385-477	US-109-438-486-26 US-10-325-810-216 US-10-053-758-26	US-09-836-073-14 US-09-843-676-26 US-09-766-253-26	US-09-836-073-13 US-09-836-073-1 US-09-836-073-5	US-09-836-073-19 US-09-836-073-4 US-09-836-073-2	ID
Sequence 26, Appl Sequence 477, App		$\sim \sim \sim$	Sequence 13, Appl Sequence 1, Appli Sequence 5, Appli	Sequence 19, Appl Sequence 4, Appli Sequence 2, Appli	Description

45	44	43	42	41	40	39	38	37	36	3 5	34	ω u	32	لد	٠ 0 د	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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7-70	-10-424-59	-96	-10-437-96	-10-767-70	61	-10-054-29	3-75	-	8-4	.253	676	73	-437-96	963-	-701-4	US-09-836-073-12	US-09-836-073-11	10-424-599	US-10-424-599-254661		US-09-836-073-17	US-09-836-073-9	œ	H	-073-15	-10-424-599-	-10-264-049-	US-10-102-806-695	
Sequence 40959, A	7	Sequence 179489,	Ø	O	e 25	25	e 25	e 21	e 25	25,	25	e 10,	e 16	Sequence 134637,		12, App1	Sequence 11, Appl	Sequence 254664,		N		9	ന		5	. 6	2643,	695	ı

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 16
TYPE: PRT
ORGANISM: Drosophila
US-09-836-073-19
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US-09-836-073-19
                                                             ; Sequence 4, Application US/09836073 ; Patent No. US20020173475A1
                                                                                                                              RESULT 2
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09836073 Patent No. US20020173475A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            Query Match 100.0%;
Beat Local Similarity 100.0%;
Ma:..hes 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dasgupta, Asim
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Pred. No. 2.2e-07;
Nismatches 0; Indels
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FILING DATE: 06-MAY-PRIOR APPLICATION DATA:

06-MAY-1997

US 08/851,843

FILING DATE: 25-APR-

PRIOR APPLICATION DATA:

09-MAY-1997

US 08/854,050

APPLICATION NUMBER:

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RESULT 15
US-08-854-050-25
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                              atent No. 6261836
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Linguer, Joachi
APPLICANT: Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 (NFORMATION FOR SEQ ID NO: 215:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                       NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                              APPLICANT: Harley, Carring H.
APPLICANT: ANOTEWS, William H.
APPLICANT: No. 6261836el Telomerase
TITLE OF INVENTION: No. 6261836el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Teo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
                                                                                                                  COUNTRY:
                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICEQIEYYFGD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIRQVEYYFGD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08854050
                                                                                                                                                                                                                                                                               Chapman, Karen b
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 amino acids
                                                                                                                                                                                                                                                                                                                             Nakamura, Toru
Chapman, Karen B.
                                                                                                                  United States of America
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                                                                                                                                                                                                                                                                                                                                                                Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER: US 08/911,312
14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US 08/912,951
14-AUG-1997
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TOPOLOGY: not relevant

MOLECULE TYPE: peptide
US-08-854-050-25
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                                                                  Query Match 57.1%; Score 48; DB 3; Best Local Similarity 72.7%; Pred. No. 0.082; Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
PILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
PILING DATE: 01-OCT-1996
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-APR-1997
CLASSIFICATION: ---
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                                 5 IIRQVEYYFGD 15
                                                                                                                                                                                                              amino acid
ICEQIEYYFGD 11
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576-0300
576-0300
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                                                                                                                                                                                                                                                                                                                                                   36,429
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                                                                      2; Indels
                                                                                                   Length 38;
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                                                                      Gaps
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Search completed: September 10, 2004, 18:05:12 Job time : 14.1229 secs

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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-721-456-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-851-843A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6093809
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08851843A
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           NUMBER OF THE PROPERTY ADDRESS:

CORRESPONDENCE ADDRESS:

Townsend and Townsend and Crew LLP

ADDRESSEE: Townsendero Center, 8th Floor
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Nakamura, Toru APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 9; Conserv
                                                      FILING DATE:
                                                                                                                                                                                                                                                               CITY: San Francisco
                                                                      APPLICATION NUMBER:
APPLICATION NUMBER:
                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
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                 APPLICATION DATA:
                                                                                                                                                                                                           94111
                                                                                                                                                                                                                                                                                                                                          I: Andrews, William H.
INVENTION: No. 6093809el Telomerase
F SEQUENCES: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/854,050
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FILING DATE: 01-OCT-1997
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APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                California
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                                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                  Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chapman,
                                                                                                                                                                                                                                                                                                                                                                                              Harley, Calvin
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                                                    06-MAY-1997
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75.0%;
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US 08/846,017
                                                                      US/08/851,843A
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Pred. No. 0.036;
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RESULT 14
US-08-974-549A-215
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APPLICANT: Nakamura, Ton...
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, William H.
TOTTICANT: ANGREWS, WILLIAM TOTTICANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 215,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                            FILING DATE: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: 01-OCT-1996
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF THE PROPERTY ADDRESS:

CORRESPONDENCE ADDRESS:

Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICATION NUMBER:
                                                                                                                                                         SOFTWARE: PatentIn Release CURRENT APPLICATION DATA: APPLICATION NUMBER: US/01 FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1. CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                               APPLICATION NUMBER: FILING DATE: 18-API
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                          CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                      California
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                                18-APR-1997
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72.7%;
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                                                                                                                                                                                                                Release #1.0,
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                                                 US 08/844,419
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ER: 015389-002930US
US 08/846,017
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                                                                                                                                                                                                                 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 38;
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Query Match
Best Local Similarity
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REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH. 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6610839
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,43
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                                                                                                                                                                                    FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 IIRQVEYYFGDF 16
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                                                                                                   APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                              APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                     APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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Morin, Gregg B.
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Andrews, William H.
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Nakamura, Toru
Chapman, Karen B.
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US 08/854,050
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US-09-721-456-214
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                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                               PRIOR APPLICATION DATA:
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                                                          APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19 NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                     APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
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Chapman, Karen B.
Morin, Gregg B.
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Query Match 59.5%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                 MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                          LENGTH: 38 amino acids
TYPE: amino acid
                                                                                                                                                                                     STRANDEDNESS: <Unknown>
       0; Mismatches
                            Score 50; DB 4;
Pred. No. 0.036;
                                                 DB 4;
       3; Indels
                                                 Length 38;
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       Gaps
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Best Local Similarity
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
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                                                                                                                                   APPLICATION NUMBER: 07/648,20 FILING DATE: January 31, 1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harley, John TITLE OF INVENTION: METH TITLE OF INVENTION: AUTO
                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION:
                                                                           FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION:
                 NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                            APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
                                                                                                                                                                                                                                                                                        FILING DATE: Jur CLASSIFICATION:
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                                                                                                               APPLICATION NUMBER: 07/472,947
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REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B: Patrea L. Pabst
2800 One Atlantic Center, 1250 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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90.9%;
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                                 31,284
                     OMRF114CIP(2)DIV
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Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
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RESULT 10
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; LOCATION:
US-08-475-955-20
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                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     FILING DATE: 18-APR-
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7:
CORRESPONDENCE ADDRESS:
                                                                            PRIOR APPLICATION DATA:
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                        FILING DATE: 25-APR-1997 PRIOR APPLICATION DATA:
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CITY: San |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 75.
APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                             APPLICATION NUMBER: FILING DATE: 14-AU
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 19-NOV
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                                                                                              FILING DATE:
                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                        APPLICATION NUMBER:
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Morin, Gregg B.
Harley, Calvin B.
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                                                                                                                                          TUMBER: US 08/851,843
06-MAY-1997
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                                                                                             09-MAY-1997
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75.0%;
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                                                               US 08/911,312
                                                                                                             US 08/854,050
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Pred. No. 0.
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RESULT 7
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GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 015389-002930US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILROVEYYFGD 11
                                                                                                                                                                                                                                    FILING DATE: 18-APK-1997,
APPLICATION NUMBER: US 08/846,017
PULING DATE: 25-APR-1997
FULING DATE: 25-APR-1997
FULING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/402,181B FILING DATE: 29-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                  APPLICATION NUMBER: WO PCT/US97/17885
                                                         FILING DATE:
                                                                                                                                                          FILING DATE: 06-MAY-1557,
APPLICATION NUMBER: US 08/854,050
PUTLING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
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                                                                         APPLICATION NUMBER: US 08/915,503
                                                                                           FILING DATE:
                                                                                                                                                                                                             APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                  APPLICATION NUMBER: US 08/911,312 PILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                PPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09402181B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94111-3834
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Harley, Calvin B.
Andrews, William H.
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
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                                                                                             14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 4;
Pred. No. 0.0021;
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US-09-721-456-216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                     APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ausenhus, Scott L. REGISTRATION NUMBER: 42,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415)
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                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 39 amino acids
                                                                                                                PPLICATION NUMBER: US 08/854,050
                                                                                                                                                    PPLICATION NUMBER: US 08/851,843
                                                                         PPLICATION NUMBER:
                                                                                               ILING DATE:
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                                                                                                                                      LING DATE:
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                  CATION NUMBER: US 08/912,951
NG DATE: 14-AUG-1997
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                         NUMBER: US 08/846,017
25-APR-1997
                                                                                             09-MAY-1997
                                                                                                                                      06-MAY-1997
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                                                                         US 08/911,312
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Pred. No.
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08/915,503
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atent NO. VALUE GENERAL INFORMATION:
GENERAL INFORMATION:
GECH, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION UNMEER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
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REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
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                                      PRIOR APPLICATION DATA:
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 06-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
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                   APPLICATION NUMBER:
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: United States of America
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                      25-APR-1997
                                                                                                                                                                                                                                                                                                                     Floppy disk
18-APR-1997
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                                                                                        US 08/846,017
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                   US 08/844,419
                                                                                                                                                               US 08/851,843
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Pred. No. 0.0021;
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GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: not
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                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews, William H.
TITLE OF INVENTION: No. 630986
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IIRQVEYYFGD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: 39 amino acids amino acid
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
 NAME: Apple, REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
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Chapman, Karen B.
Morin, Gregg B.
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90.9%;
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Randolph T.
NUMBER: 36,4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1997-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )RGANISM: Artificial Sequence
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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APPLICATION NUMBER: US/
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                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                              CLASSIFICATION:
                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 18-APR-1997
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Two Embarcadero Center, 8th Floor
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Nakamura, Karen B.
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                                                                                                              01-OCT-1996
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06-MAY-1997
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                                                                                                                                 US 08/724,643
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Pred. No. 0.00085;
1; Mismatches 4
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US-08-974-549A-216
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Best Local Similarity
Matches 10; Conserv
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19-NOV-19
CLASSIFICATION: 536
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-OCT-
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 1
FILING DATE: 09-MAY-
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APPLICATION NUMBER: U
FILING DATE: 06-MAY-
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/724,643
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TILE OF INVENTION: Human Telomerase Catalytic Subunit
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SOFTWARE: Patentin Patent
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                                                                                          APPLICATION NUMBER: FILING DATE: 14-AUC
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California
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Two Embarcadero Center, Eighth Floor
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Harley, Calvin B.
Andrews, William H
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Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US 08/846,017
25-APR-1997
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                                                                                                                                                                                    UMBER: US 08/911,312
14-AUG-1997
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                                                                                          UMBER: US 08/912,951
14-AUG-1997
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06-MAY-1997
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MBER: US 08/915,503
14-AUG-1997
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and is derived by analysis of the total score distribution
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     greater
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84
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Match Length
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| (cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
| (cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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               US-09-316-630-3

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US-08-971-849A-216

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US-09-403-181B-216

US-09-402-181B-216

US-09-402-181B-214

US-09-402-181B-214

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US-09-402-181B-215

US-08-974-549A-25

US-08-974-549A-25

US-08-974-549A-215

US-09-420-181B-215

US-09-420-181B-215

US-09-430-323-25

US-09-402-181B-215

US-08-851-843A-24

US-08-851-843A-27

US-08-951-843A-27

US-08-951-843A-27

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Compugen Ltd.
Sequence 3, Appli
Sequence 4, Appli
Sequence 26, Appl
Sequence 216, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 216, Appl
Sequence 216, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 217, Appl
Sequence 27, Appl
Sequence 217, Appl
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42 50.0 167 4 US-09-134-0UCC-3435 41 48.8 74 4 US-09-439-554-6 41 48.8 141 4 US-09-439-554-24 41 48.8 292 4 US-09-439-554-24 40.5 48.2 2710 2 US-08-680-459A-12 40.5 48.2 2710 2 US-08-680-459A-12 40.5 48.2 2710 2 US-08-487-8268-12 40.5 48.2 2710 2 US-08-487-8268-12 40.5 48.2 2710 2 US-08-487-8268-12 40.4 47.6 376 4 US-09-49-039A-11743 40 47.6 506 4 US-09-672-785-8 40 47.6 506 4 US-09-672-785-8 40 47.6 512 4 US-09-672-785-8 40 47.6 1145 4 US-09-470-443-6 40 47.6 1145 4 US-09-470-443-6 40 47.6 1145 4 US-09-970-43-2 40 47.6 3571 4 US-09-911-842A-2 40 47.6 3571 4 US-09-671-7385 46.4 319 4 US-09-672-976-7385	Д	44	43	42	41	40	9	38	ام) ت	36	35	34	33	32	31	30	29	28
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	29238, F	7385, Ap	2, Appli	4, Appli	2, Appli	6, Appli	4, Appli	8, Appii	2, Appli	11743, A	14, Appl	12, Appi	12, Appi	12, Appi	24, App1	×	6, Appli	SESS, AD

ALIGNMENTS

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; OTHER INFORMATION: Description of Artificial Sequence:
US-09-316-630-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
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US-09-316-630-3
                                                                                                                                                                Sequence 4, Application US/09316630 Patent No. 6291637 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
SEQ ID NO 3
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                 APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERPERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIC
FILE REFERENCE: 22000-20548.21
CURRENT PPPLICATION NUMBER: US/99/316,630
CURRENT FILING DATE: 1999-05-21
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APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL
TITLE OF INVENTION: SMALL YEAST RNA REVEALS
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                       EAKICHQIEYYFGDF
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66.7%;
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                                                                                       CRITICAL RNA-PROTEIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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Search completed: September 10, 2004, 17:51:56 Job time: 51.1559 secs
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                                                                                                                                                                                                                                                                                                                                               Query Match 67.9
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 408 AA;
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RESULT 14
ADD46272
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Best Local S
Matches 10
                The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2001;
01-NOV-2001;
26-NOV-2001;
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polynucleotides, a
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                                                                                                                                                                                                                                                                                                                                                                                 preparing
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2001US-0346382P.
2001US-0333347P.
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for producing
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Pred. No.
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pain in an animal.
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pharmaceutical
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that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal times of a first sequence claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent

The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also

fragment,

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New composition comprising medicament for

two or mo

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nore isolated ; y pain in an a

d polypeptides, useful for animal.

Claim 1; Page; 1017pp; English

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                         14-AUG-2001;
01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                       spinal
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                                                                                                                                                                                                    Woolf C,
                                                                                                                                                                                                                         (GEHO )
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segmental nerve injury; chronic cons
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BAYER AG.
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2001US-0346382P.
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Pred. No. 0.18;
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The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, appotosis, bathological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-2000; 2000GB-00030076.
08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2002
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Pred. No. 0.18
1; Mismatches
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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a activity in an animal of one or more of the polynucleotides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more or more polynucleotides or their antibodies. The polynucleotide or the compound that
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spinal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                                       Claim 1; Page; 1017pp;
                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                      Woolf C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002WO-US025765
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9937.
                                                                                                                                                                                                                                                                                                                                                                                                        Costigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constriction injury; CCI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .18;
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RESULT 10
AAG01351
ID AAG01351
XX AAG01
XX AAG01
XX O6-OC
XX Human
XX Human
XX Human
XX Homo
XX Gene
XX Gene
XX EP103
XX EP103
XX 21-FE
XX 26-FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral life cycle; antiviral therapy; pharmaceutical; veterinary;
agricultural; horticultural; virucide; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2002; 2002WO-US011589.
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                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                          06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-058634/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dasgupta A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2001;
                                                                                                                   06-SEP-2000
                                                                                                                                           EP1033401-A2
                                                                                                                                                                                                                                                                                   AAG01351;
                                                                                                                                                                                                                                                                                                           AAG01351 standard;
              Dumas Milne Edwards J,
                                                                                          21-FEB-2000;
                                       (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                          therapy;
                                                                                                                                                                                                                                  secreted
                                                                                                                                                                                                        5' EST; expressed
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EAKICHQIEYYFGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-00836073
                                                                                                                                                                                                                                                          (first entry)
                                                                                          2000EP-00200610
                                                                                                                                                                                            chromosome mapping.
                                                                                                                                                                                                                                 protein,
                                                                99US-0122487P
                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                        67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baidya N;
                                                                                                                                                                                                                                 SEQ ID NO:
             Duclert A,
                                                                                                                                                                                                        sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 6;
Pred. No. 0.0048;
1; Mismatches
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                                                                                                                                                                                                                                    5432.
              Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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RESULT 11
AAW03716
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and even in those cases where therefore be used to obtain full length cDNAs are genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500381/45.
N-PSDB; AAC01357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
                                                                                        Auto-antigen U2-RNP, associated with severe overlap syndrome - useful for diagnosis and
                                                                                                                                   WPI; 1996-362015/36
                                                                                                                                                                                                                     31-DEC-1984;
                                                                                                                                                                                                                                             27-MAY-1987;
                                                                                                                                                                                                                                                                        30-JUL-1996.
                                                                                                                                                                                                                                                                                                  US5541291-A.
                                                                                                                                                                                                                                                                                                                                                        systemic lupus
                                                                                                                                                                                                                                                                                                                                                                      Autoimmune disease; La autoantigen; Sjogren's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                             Human autoantigen La(SS-B).
                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW03716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW03716 standard; protein;
                                                                                                                                                                                          (UYDU-) UNIV
                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                          DUKE
                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                                                                                                   84US-00687908
                                                                                                                                                                                                                                                87US-00054871
                                                                                                                                                                                                                                                                                                                                                         erythematosus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                             polymyositis-scleroderma treatment of autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mapping procedures.
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The human lupus antigen (La) is diagnostic for Sjogren's syndrome, as well as occurring in systemic lupus erthematosus patients. The La prois clinically related to the Ro protein that is highly common among

The La protein

Disclosure; Col 15-16; 21pp; English.

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RESULT 7
ABG72101
                                                                    Query Match
Best Local S
Matches 10
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Best Local (
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                                                                                                                                                                                                The present invention relates to peptides and methods of inhibiting the regalication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blockemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease virus, echo virus, hepatitis C virus, infectious bronchitis virus, di and human hepatitis B virus, and vesicular stomatitis virus. The pepalso inhibits replication of the above viruses. The LAP peptide selectively inhibits viral protein translation, and is therefore not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal ribosome entry site initiated translation; La antigen prival life cycle; antiviral therapy; pharmaceutical; veterinary agricultural; horticultural; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viral replication inhibitor, IRES initiated translation, LAP, internal ribosome entry site initiated translation, La antige
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                                                                                                                                                          Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral therapy in pharmaceutical, vet agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound containing acidic and aromatic amino acids, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dasgupta A,
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ERAIIRQVEYYFGDF
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                         67.9%;
66.7%;
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                                                                 Score 57; DB 6;
Pred. No. 0.0048;
1; Mismatches
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Pred. No.
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L; Mismatches
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                                                                      4.
                                                                                                                Length 18;
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Viral replication internal ribosome

inhibitor; entry site

IRES initiated translation; LAP; initiated translation; La antige

antigen

protein;

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Matches
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                                     Viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound containing acidic and aromatic amino acids, antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal ribosome viral life cycle; agricultural; hort
                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 14; 19pp; English.
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                                                                                                                ABG72114 standard; peptide; 18
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entry site initiated translation; La antigen protein;
antiviral therapy; pharmaceutical; veterinary;
ticultural; virucide.
                                     inhibiting
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0.0048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen p viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide; mouse.
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ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; Page 16; 19pp; English.
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New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
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Pred. No. 0.0032;
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                                                                                                                                                                                                                          PRESIDENT
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                                                                                                                                                                                                                                                                                                                                                                                                               viral replication; IRNA; antiviral agent; picornavirus; flavivirus; coronavirus; hepatitis virus; rhabdovirus; adenovirus; coxsackie virus; parainfluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus; foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral replication;
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                                                                                                                                                                                                                                                                                 22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal ribosome entry site; IRES; translation;
RNA; antiviral agent; picornavirus; flavivirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide (LAP).
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0.0045;
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This sequence is the La autoantigen binding domain (LAP). LAP is a cellular protein which binds to an internal ribosome entry site (IRES). The peptide is used to inhibit mRNA translation, viral protein translation or viral replication. Viral mRNA translation is initiated at the IRES and the LAP peptide prevents translation initiation factors from binding at the site. The peptide can be used alone or in combination with an inhibitor RNA (IRNA see AAZ45200). The LAP peptide is useful as an antiviral agent, which works through the inhibition of mRNA translation, especially viral mRNA. Examples of viruses which can be inhibited are picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses, rhabdovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,

with from translation

Page 57; 81pp; English.

WPI;

2000-062712/05.

New yeast inhibitory peptide useful for inhibiting

viral protein

and replication.

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RESULT 2
ABB65316
AC ABB6
XX ABB6
AC ABG6
AC ABB6
AC A
                                            RESULT 3
ABG72104
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                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABLI6176-ABLI6177), expressed DNA sequences (ABLI61840-ABLI6175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 22740; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic a genes from Drosophila
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11-JUL-2000; 2000US-00614150
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                  standard; peptide;
                                                                                                                                                  QERAITRQVEYYFGD
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Pred. No.
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Pred. No. 7.1e-08;
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RESULT 4
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ID ABG7
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral replication inhibitor; IRBS initiated translation; LAP; internal ribosome entry site initiated translation; La antigen viral life cycle, antiviral therapy; pharmaceutical; veterinary agricultural; horticultural; virucide.
                                                                Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen p viral life cycle, antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 16; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
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                                       Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                 inhibiting
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                                                                                                                                 peptide,
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Pred. No.
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0.00063;
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Minimum
Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                             Title:
                                                                                                                            Database
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Maximum Match 100%
Listing first 45 summaries
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84
                                                                                          A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
                                                                                                                                                                                                                                                                                                  1586107 seqs, 282547505 residues
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Copyright (c) 1993 - 2004 Compugen Ltd.
geneseqp2002s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	ı a ĸ	Length	S B	ID	Description
NI	78	92.9	390	4.	ABB65316	Ab565316
ω	62		ш	σ	ABG72104	Abg72104
4	58		18	σ	ABG72102	Abg72102
ហ	57	•	17	σ	ABG72113	Abg72113
თ .	57	67.9	18	w	AAY52200	Aay52200
7	57	•	18	9	ABG72101	Abg72101
œ	57	.7	18	6	ABG72105	Abg72105
ø	57		18	σ	ABG72114	Abg72114
10	57		92	w	AAG01351	Aag01351
11	57	7.	408	N	AAW03716	Aaw03716
12	57	•	408	σ	ABP65252	Abp65252
13	57	7.	408	7	ADE63991	Ade63991
14	57	67.9	408	7	ADD46272	Add46272
15	57	7.	408	7	ADE63995	Ade63995
16	57	7.	408	7	ADE62859 ·	Ade62859
17	57	67.9	415	7	ADE63989	Ade63989
18	57		415	7	ADE63993	Ade63993
19	57	67.9	439	4	ABG08417	Abg08417
20	57		460	w	AAB58987	Aab58987
21	57		460	v	ABP41511	Abp41511
22	54		18	6	ABG72115	Abg72115
23	54		21	2	AAR43394	Aar43394
24	53	63.1	411	σ	ABP70526	Abp70526
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42	42	43	43	44	44	44	44	44.5	45	46.5	47	47	47	47	48	48	49	49	50
50.0	50.0	51.2	51.2	52.4	52.4	52.4	52.4	53.0	53.6	55.4	56.0	56.0	56.0	56.0	57.1	57.1	58.3	58.3	59.5
275	18	979	466	315	315	315	315	18	18	19	1379	993	923	913	483	18	18	18	18
σ	σ	7	σ	7	7	7	7	თ	σ	σ	4.	w	w	w	ω	σ	σ	σ	o
ABR52759	ABG72107	ADB64292	ABR52760	ADE56773	ADE56777	ADE62044	ADE62048	ABG72118	ABG72103	ABG72116	ABB68940	AAG47712	AAG47713	AAG47714	AAG29675	ABG72110	ABG72112	ABG72111	ABG72117
Abr52759	Abg72107	Adb64292	Abr52760		7	4.				9				Aag47714	Aag29675	Abg72110	Abg72112		`
Protein s	Viral rep		Protein s	Rat Prote				Viral rep		Viral rep	Drosophil	Arabidops	Arabidops	Arabidops	Arabidops	Viral rep	•		ATTUT TEN

ALIGNMENTS

RESULT 1 Viral replication inhibiting peptide, DROSOPHILA 28-JAN-2003 ABG72119 standard; peptide; 16 ABG72119; (first entry) A

Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide.

Drosophila sp.

WO200283858-A2

24-OCT-2002.

12-APR-2002; 2002WO-US011589.

16-APR-2001; 2001US-00836073.

(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

Dasgupta A, Das S, Baidya N;

WPI; 2003-058634/05.

New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.

Claim 1; Page 15; 19pp; English.

XAXFXBXBXBXBXBXFXFXFXFXFXBXSSSSSSSSXSXX The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 16 AA;

This Parae-Binokk (USBin)

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APPLICANT: KAWASAKI, GLENN
APPLICANT: WBBB, HEATHER K.
APPLICANT: OWENS, JEFFREY
APPLICANT: LIEDTKE, RAYMOND
APPLICANT: LIEDTKE, RAYMOND
APPLICANT: LIEDTKE, RAYMOND
APPLICANT: LIEDTKE, DOREEN
APPLICANT: LIEDTKE, MARK
APPLICANT: LIEGAZ, MARK
APPLICANT: LIEGAZ, MARK
APPLICANT: LAWSON, SOBOMABO
TITLE OF INVERTION ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE
FILE REFERENCE: 30865
CURRENT APPLICATION NUMBER: US/10/651,183
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US/10/12,762
PRIOR APPLICATION NUMBER: 00/163,126
PRIOR FILING DATE: 199-11-02
PRIOR PILING DATE: 199-11-02
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 00/704,036
PRIOR APPLICATION NUMBER: 60/203,349
PRIOR PILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 1252
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-651-183-20
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US-10-651-183-20
Sequence 20, Application US/10651183
Publication No. US20040096929A1
GENERAL INFORMATION:
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Search completed: September 10, 2004, 18:11:57 Job time : 40.424 secs
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Matches 10; Conserv
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                                                                                                                                                                    47.8%; Score 43; DB 16; Length 1252; ilarity 58.8%; Pred. No. 2.3e+02; Conservative 2; Mismatches 5; Indels
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61 ISKGNLGRÍRKEFÝFG 76

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RESULT 12
US-10-464-811-20
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                                                                                                           ; TYPE: PRT ; ORGANISM: Saccharomyces cerevisiae US-10-464-811-20
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                                                                                                                                                            APPLICANT: Kraus, Jana
APPLICANT: Oliveriusova, Jana
APPLICANT: Oliveriusova, Jana
APPLICANT: Oliveriusova, Jana
APPLICANT: Oliveriusova, Jana
TITLE OF INVENTION: Human Cystathionine B-Synthase Variants and Methods of Production
CURRENT REFERENCE: 22048-49
CURRENT APPLICATION NUMBER: US/10/464,811
CURRENT FILING DATE: 2003-06-17
PRIOR APPLICATION NUMBER: 60/389,541
PRIOR FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/10464811 Publication No. US20040033219A1 GENERAL INFORMATION:
                                               Query Match
Best Local Similarity
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Best Local Similarity
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                                      Matches
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/171,100 PRIOR FILING DATE: 1999-12-16 NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: nucleosides
FILE REFERENCE: BASF-NAE-1331-99-US
CURRENT APPLICATION NUMBER: US/09/734,017A
CURRENT FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved TITLE OF INVENTION: the TITLE OF INVENTION: synthesis of amino acids, vitamins, cofactors, nucleotides and TITLE OF INVENTION: nucleosides
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TYPE: PRT
ORGANISM: Physcomitrella patens
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2 SKLEASTIRQEYYFGDA 18
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US20020142422A1
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Ehrhardt, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duwenig, Elke
Schmidt, Ralf-Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frank,
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                                    Conservative
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                                                   47.8%;
58.8%;
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41.2%;
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Pred. No.
                                                     Score 43;
Pred. No.
                                    Mismatches
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26;
                                                       DB
82;
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                                                                      Length 507;
                                    Indels
                                  0;
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                                  Gaps
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; TYPE: PRT
; ORGANIEM: Saccharomyces cerevisiae
US-10-451-467A-182
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                                                              ; LENGTH: 1252
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-012-762-20
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CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: EP 00870318.3
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR APPLICATION NUMBER: EP 01870003.9
PRIOR FILING DATE: 2001-01-09
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TENGTH: 507
Query Match
Best Local Similarity
                                                                                                                                                      SOFTWARE: PatentIn version 3.1 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/10012762 Publication No. US20030138872A1
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Best Local Similarity
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                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/163,126
PRIOR TILING DATE: 1999-11-02
PRIOR APPLICATION NUMBER: 09/704,036
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/203,349
PRIOR FILING DATE: 2000-5-10
NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 30865
CURRENT APPLICATION NUMBER: US/10/012,762
CURRENT FILING DATE: 2002-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WEBB, HEATHER K.
APPLICANT: ORDENS, JEFFREY
APPLICANT: LIEDTKS, FAYWOND
APPLICANT: LIEDTKS, RAYWOND
APPLICANT: FOREST, DOREEN
APPLICANT: LEGAZ, MARK
APPLICANT: LEGAZ, MARK
APPLICANT: LAWSON, SOBOMABO
TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KAWASAKI, GLENN
APPLICANT: WEBB, HEATHER I
APPLICANT: OWENS, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REEKMANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: LUYTEN, WALTER HERMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
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58.8%;
47.8%;
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Score 43;
Pred. No.
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DB 14;
2.3e+02;
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                    Length 1252;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695
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US-10-264-049-2643
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                                                                                                                                  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 128214
LENGTH: 169
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SEQ ID NO 2643
LENGTH: 460
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Best Local Similarity
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
                                                                                                                                                                                                                                                                                           APPLICANT:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA13391
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                               APPLICANT:
                       NAME/KEY: unsure
LOCATION: (1)..(169)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
OTHER INFORMATION: Clone ID: PAT_MRT4530_3058C.1.pep
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                                                                                                                                                                                                                                                                                                                                    Zhou, xi...
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Wu, Wei
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55.6%;
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Pred. No. 6
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Pred. No. 6
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Best Local Similarity
"---hes 8; Conserv
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; OTHER INFORMATION: Clone ID: 700337382_FLI.pep
US-10-425-114-37684
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Query Match
Best Local Similarity
"hes 8; Conserva
                                                                                             , OTHER INFORMATION: Clone ID: UC-ZMROMO17113D10_FLI.pep US-10-425-114-71728
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LENGTH: 172
TYPE: PRT
CHANGEN Zea mays
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37694
LENGTH: 172
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Best Local Similarity 30.8%;
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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ORGANISM: Zea mays
                                                                                                                                   FEATURE:
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                47.8%;
nilarity 50.0%;
Conservative
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50.0%;
                  ; Score 43; DB
; Pred. No. 24;
3; Mismatches
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                        12;
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                                                      Length 172;
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Best Local Similarity 71.4
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
S-09-836-073-2
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SOPTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 16
TYPE: PRT
                                                                                                                                                                                                                                    Sequence 477, Application US/10170385
Publication No. US20030203372A1
GENERAL INFORMATION:
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                                                                                        APPLICANT:
APPLICANT:
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                 APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
                                                                                                                                                 APPLICANT:
                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                 APPLICANT: Ward, Neil Raymond APPLICANT: Mundy, Christopher
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TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
CURRENT APPLICATION NUMBER: US/10/170,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                        Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                            Harris, Robert Alan
White, Jonathan
                                                                     Kingsman, Susan Mary
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                                                                                                                                                                                                   Christopher Robert
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66.7%; Pred. No. 1.5;
Ltive 1; Mismatches
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Pred. No. 0.
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CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 695
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US-10-102-806-695
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                                  CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
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Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO3
                                                                                                                                                                                                                                                                    Sequence 695, Application US/10102806 Publication No. US20030054421A1 GENERAL INFORMATION:
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LENGTH: 408
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SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 695
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PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OP INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PIC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
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Local Similarity 55.6%;
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Pred. No. 53;
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Pred. No. 6
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Perfect score:
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Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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143.151 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
/ cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB-COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB-COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUB-COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUB-COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09B_PUB-COMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US09B_PUB-COMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10B_PUB-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 3 4 4 5	90 re 44.3.5	Query Match 100.0 49.4 48.3 48.3 48.3	Query Match Length Match Length 100.0 18 49.4 16 48.3 18 48.3 460 48.3 460	DB 9 9 112 112 112 113 114 115 115 115 115 115 115 115 115 115	ID US-09-836-073-18 US-09-836-073-19 US-09-836-073-2 US-10-170-385-477 US-10-170-385-477 US-09-925-298-695 US-10-102-806-695 US-10-264-049-2643	Description Sequence 18, App Sequence 2, Appl Sequence 477, A Sequence 695, A Sequence 695, A Sequence 695, A Sequence 695, A
	44 43 43 43 43 43 43 5 5	100.0 49.4 48.3 48.3 48.3	18 16 18 408 460 460	11111111111111111111111111111111111111	US-09-836-073-18 US-09-836-073-19 US-09-836-073-2 US-10-170-33-477 US-09-925-298-695 US-10-102-806-695 US-10-102-806-695 US-10-264-049-2643	
	43.5 43	48.3 47 8	460 169	15	US-10-264-049-2643 US-10-437-963-128214	
	43	47.8	172	12	US-10-425-114-37684	
0	43	47.8	172	12	US-10-425-114-71728	
11	43	47.8	184	9	US-09-734-017A-32	Sequence 32, Appl
12	43	47.8	507	12	US-10-464-811-20	Sequence 20,
13	43	47.8	507	16	US-10-451-467A-182	Sequence
14	43	47.8	1252	14	US-10-012-762-20	
μ 5	43	47.8	1252	7	115-10-651-183-20	

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12	9	12	12	12	12	15	14	12	15	16	15	14	14	14	10	9	9	9	14	14	14	12	10	9	ø	9			
-282	US-09-815-242-5432	US-10-425-114-57809	US-10-425-114-68939	US-10-425-114-69655	0-282-122		US-10-177-478-8	US-10-282-122A-47032	US-10-369-493-3398	US-10-437-963-147678	US-10-369-493-8277	US-10-054-611-24	US-10-054-295-24	US-10-053-758-24	US-09-438-486-24	US-09-766-253-24	US-09-843-676-24	US-09-836-073-16	US-10-054-611-26	US-10-054-295-26	US-10-053-758-26	O	US-09-438-486-26	US-09-766-253-26	US-09-843-676-26		ė	US-09-836-073-1	US-09-836-073-13
e 43838	Sequence 5432, Ap	57809	•	Sequence 69655, A	44539,		8, App	47032,		147678		24,	24,	24	-		•	`.	٠,	~	•	Sequence 216, App	Sequence 26, Appl	Sequence 26, Appl	26	Sequence 14, Appl	9	,	Sequence 13, Appl

ALIGNMENTS

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APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Dasidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054822
CURRENT APPLICATION UNMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENCTH: 18
TYPE: PRT
ORGANISM. MOGNIST
                                                                                                           RESULT 2
US-09-836-073-19
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                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mosquito US-09-836-073-18
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Sequence 19, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09836073 Patent No. US20020173475A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                          100.0%; Score 90; DB 9; 1; al Similarity 100.0%; Pred. No. 1.3e-08; 18; Conservative 0; Mismatches 0;
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PRIOR APPLICATION : .......

PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
REGISTRATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: APPLICATION: SEQ 1D NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

46.7%; Score 42; DB 4; Ler
0;
                                                           ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8030
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-328-352-8030
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                                                                                                                             CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8030
LENGTH: 287
                                                                                                                                                                                                                                       Sequence 8030, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 46.7%; Sometive 100.0%; I Matches 7; Conservative 0;
Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 QEYYFGD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 QEYYFGD 10
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44.4%;
57.1%;
  Score 40;
Pred. No.
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  DB 4;
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                       Length 287;
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Matches 8; Conservative 1; Mismatches

Qy 2 SKLEASTIRQEYF 15

Db 170 SKQEEITIKDRYYF 183
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Indels

<u>,</u>

Gaps

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Search completed: September 10, 2004, 18:05:12 Job time : 16.8883 secs

PPLICANT:

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RESULT 13
US-08-854-050-24
; Sequence 24, Ag
; Patent No. 626)
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Best Local S
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                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 24:
                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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APPLICATION NUMBER: 1
FILING DATE: 25-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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7; Conserva
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                                                                                                                                 4, Application US/08854050
6261836
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Chapman, Karen B.
                                             Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
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 Andrews, William H.
                                                                                             Cech, Thomas R.
             Morin, Gregg B.
Harley, Calvin
                                                                             Lingner, Joachim
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25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
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US-09-430-323-24
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                                                                                                                                                    Sequence 24, Application Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-MAY-199,
FILING DATE: 09-MAY-199,
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1wo CITY: San Francisco
CITY: San Francisco
STATE: California
""-i+ed Stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IMP C COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                      APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                           11 QEYYFGD 17
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Two Embarcadero
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3: peptide
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                                                                                                                   ingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
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100.0%;
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225
                                                                                                                                    Thomas R.
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Query Match
Best Local Similarity
Thes 9; Conserve
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US-09-721-456-216
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                                                                                                                   Sequence 216, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
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                                                                                                                                                                                                                                                                                     LROVEYYFGDA 12
                                                                                                                                                                                                                                                                                                                           IRQ-EYYFGDA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version NT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCE CHARACTERISTICS:
LENGTH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                        Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                Morin, Gregg B.
Harley, Calvin B.
Andrews, William H
                                                                                                                                                                                                                                                                                                                                                                                      47.2%;
81.8%;
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STRANDEDNESS: <Unknown>
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TOPOLOGY: linear
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MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID
US-09-721-456-216
                                                                              Best Loc
Matches
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-AUG-1997
APPLICATION NUMBER: W0 PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: W0 PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 015389-002610US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
                                        9 IRQ-EYYFGDA 18
                                                                                Similarity
9; Conserv
LRQVEYYFGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/721,456 FILING DATE: 22-No. 6617110-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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                                                                                Conservative
                                                                                                                                                                                                                                                                                      39 amino acids
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                                                                                                    47.2%;
81.8%;
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                                                                                Score 42.5; DB
Pred. No. 0.91;
1; Mismatches
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                                                                                                                                                                                    NO:
                                                                                                                                                                                    216:
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RESULT 12 US-08-851-843A-24

Sequence 24, Application US/08851843A Patent No. 6093809 GEMERAL INFORMATION: APPLICANT: Cech, Thomas R.

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                                                                                                 US-09-430-323-26
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                                             Sequence 26, Application Patent No. 6309867
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                               TYPE: amino acids
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
OLECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: 1
FILING DATE: 18-APR-
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
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CLASSIFICATION: 536
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STATE: California
                                                                                                                                                                                                                                               Local
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APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
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                                                                                                                                                                                                                              Similarity 9; Conserv
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                                                                                  Application US/09430323
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996
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                                                                                                                                                                                                                                                                                                            peptide
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US-09-402-181B-216
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Best Local (
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; TOPOLOGY: not relevant ; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-430-323-26
                                                                                                                                                                   Sequence 216, Application US/09402181B Patent No. 6610839 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CILORIES POCT-1999
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TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                    2 LRQVEYYFGDA 12
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                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
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Morin, Gregg B.
Harley, Calvin
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81.8%;
                                                                                                                                                Thomas R
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REGISTRATION NUMBER: 36,429
REFERENCE DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      Sequence 216, Application US/08974549A Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION UNIMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                               APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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COMPUTER READABLE FORM:
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                                                   CORRESPONDENCE ADDRESS:
                                                                        NUMBER OF SEQUENCES:
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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               ADDRESSEE:
STREET: T
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San Francisco
                                                                                                                                                                                                                                                                                                                                                                  LROVEYYFGDA 12
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             3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
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06-MAY-1997
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BER: 015389-002930US
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Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.5; DB Pred. No. 0.91; Mismatches
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US-08-854-050-26

Sequence 26, Applicat Patent No. 6261836 GENERAL INFORMATION:

Application US/08854050

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APPLICANT: Cech, Thomas R.

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RESULT 8
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                                                                                                                          Matches
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 019
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Te
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/915,503
PRILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-AUG-199/
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/912,951
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PRIOR APPLICATION NUMBER: US 08/911,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-OCT-PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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FILING DATE: 18-APR-1997
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FTI.ING DATE: 01-OCT-1996
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01-OCT-1997
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                                                                                                                                          47.2%;
81.8%;
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                                                                                                                                          Score 42.5; DB Pred. No. 0.91;
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; ORGANISM: Saccharomyces cerevisiae
US-10-012-762-20
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                                                                                                                                                                                                                                                          RESULT 4
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PRIOR APPLICATION NUMBER: 60/163,126
PRIOR FILING DATE: 1999-11-02
PRIOR PPLICATION NUMBER: 09/704,036
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/203,349
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 21
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PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 1252
                                                                                                                                                                                             Sequence 3, Application US/09316630 Patent No. 6291637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 20 LENGTH: 1252
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Best Local (
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Best Local Similarity
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
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ORGANISM: Saccharomyces cerevisiae
-09-704-036B-20
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CURRENT APPLICATION NUMBER: US/09/704,036B
CURRENT FILING DATE: 2000-11-01
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TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                   589 SKLEASTTKYADVFGNA 605
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5. 6664073
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OWENS, JEFFREY
LIEDTKE, RAYMOND
FOREST, DOREEN
LEGAZ, MARK
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Sequence 20 Patent No.

26, Application US/08851843A o. 6093809

GENERAL INFORMATION: APPLICANT: Cech,

Cech, Thomas R

APPLICANT:
APPLICANT:

Lingner, Joachim Nakamura, Toru Chapman, Karen B. Morin, Gregg B. Harley, Calvin

APPLICANT:

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PRIOR APPLICATION NUMBER: 08/32:
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/08
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
RESULT 6
US-08-851-843A-26
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LENGTH: 18
TYPE: PRT
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548.21
CURRENT EPLLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
RUMBER OF SEQ ID NOS: 4
COMMUNICATION SECONDARY OF THE CONTROL 
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
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                                                                                                                                                     LEAKICHQIEYYFGD 17
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66.7%;
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Pred. No. 0.37;
0; Mismatches
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Title:
Perfect score:
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-08-951-843A-26

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US-08-785-071A-2

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US-08-849-480A-5

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	214, App	25, App1	120, App1	3910, Ap	3600, Ap	2, Appli	54, Appl	-	54, Appl	54, Appi	54, Appl	54, App1	3, Appli	2, Appli	7, Appli	7, Appli	7662, Ap	1000

ALIGNMENTS

Sectionce 4980, Application US/09134001C Patent No. 6380370 REMERAL INFORMATION: APPLICANT: Lynn Dougette-Stamm et al APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC TITLE OF INVENTION: DEIDERWIDIS FOR DIAGNOST FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 GENERAL INFORMATION: APPLICANT: KAMASAKI, GLENN APPLICANT: WEBB, HEATHER K. APPLICANT: OWERS, JEFFREY APPLICANT: LIEDTKE, RAYMONI APPLICANT: FOREST, DOREEN APPLICANT: LEGAZ, WARK APPLICANT: LEGAZ, WARK APPLICANT: LEGAZ, WARK APPLICANT: WEBB, HEATHER K. APPLICANT: OWENS, JEFFREY APPLICANT: LIEDTKE, RAYMOND APPLICANT: LIEDTKE, RAYMOND APPLICANT: LEGAZ, MARK APPLICANT: LEGAZ, MARK APPLICANT: LAWSON, SOBOMABO TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FO FILE REFERENCE: 30865 CURRENT APPLICATION NUMBER: US/10/012,762 CURRENT FILING DATE: 2002-09-26 PRIOR APPLICATION NUMBER: 60/163,126 PRIOR FILING DATE: 1999-11-02 PRIOR APPLICATION NUMBER: 09/704,036 US-10-012-762-20 ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4980 NUMBER OF SEQ ID NOS: 5674 SEQ ID NO 4980 LENGTH: 136 TYPE: PRT Sequence 20, Application US/10012762 Patent No. 6635438 98 1 VSKLEAST-IRQEYYFGDA 18 Similarity ISKLRSETDERQVYYFFDA 116 48.3%; ilarity 57.9%; Conservative 2 Score 43.5; D Pred. No. 2.6; 2; Mismatches AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS DIAGNOSTICS AND THERAPEUTICS . 6 BB FOR HOMOCYSTEINE AND CYSTATHIONINE Length 136; Indels 1: Gaps 1

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Rat Protein P38656, SEQ ID NO 9935

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Matches
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                          polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjects to the sequence of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjects.
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GENBANK; P38656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 1017pp; English.
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                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                          1 VSKLEASTIRQ-EYYFGD 17
                                                                                                                                                                                           Similarity
MAALEAKICHQIEYYFGD 27
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Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                         Human Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electronic form directly from WIPO at
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derivative or allelic variation of the nucleic acid sequence. Also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynuclectides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition composition compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynuclectide or the compound that modulates its activity is useful for preparing a medicament for treating and a pharmaceutical composition comprising the one or more that its activity is useful for preparing a medicament for treating and the compound that the compound that the compound that according to the compound that the compound that according the compound that the compound that according the compound that the compound that the compound that according the compound that the compound that the compound that according the compound that t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising the vector, a method for localityly a university which is differentially regulated in an animal subjected to pain and which is differentially regulated in an animal subjected to pain and which is differentially regulated.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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10; Conserv
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MAALEAKICHQIEYYFGD
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Pred. No. 49;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Protein P05455, SEQ ID NO 11947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 408 AA;
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14-AUG-2001; 2001US-0312147P
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segmental nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                                                                        injury; SNI; Chung.
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55.6%;
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Pred. No. 49;
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Query Match Best Local Matches

Similarity

48.3%;

Score 43.5; Pred. No. 49 Mismatches

BB 7; 5

Length 408; Indels

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Conservative

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cc subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially cc expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the cc polynucleotides, a method for producing a pharmaceutical composition, a cc polynucleotides, a method for producing a pharmaceutical composition, a crivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more compound useful in treating compoundates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction cinjury (CCI) and spared nerve injury (Chung), chronic constriction the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal that is differentially expressed in neuronal tissue of a first animal
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26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence.
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Sequence 408
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(FARB )
                                              ftp.wipo.int/pub/published_pct_sequences.
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RESULT 13
ADE63995
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                                                   Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI;
                                                                                 Human Protein P05455, SEQ ID NO 9941.
                                                                                                                     ADE63995;
                                                                                                                                      ADE63995 standard; protein;
                          Homo sapiens
                                                                                                                                                                                   10 MAALEAKICHQIEYYFGD
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                                            injury; SNI; Chung.
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WO2003016475-A2

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RESULT 10
ABP65252
ID ABP65
XX ABP65
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XX T2-NO
DT 12-NO
XX CYtos
KW CYtos
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KW ischa
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                                                                                                                                                         Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing;
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08-DEC-2000;
08-FEB-2001;
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                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                         Hypoxia-regulated
                                                                                                                                                                                                                                                                       12-NOV-2002
                                                                                                                                                                                                                                                                                                 ABP65252;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 15-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma overlap syndrome - useful for diagnosis and treatment of autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human autoantigen La(SS-B)
                                       10-DEC-2001;
                                                                  13-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYDU-) UNIV
                                                                                                                                              inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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2000GB-00030076.
2001GB-00003156.
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                                                                                                                                                                                                                                                                       (first entry)
                                       2001WO-GB005458
                                                                                                                                               erythropoiesis; hair loss; human
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                                                                                                                                                                                                                                          protein #126.
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55.6%;
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                                                                                                                                                                                                                                                                                                                           408
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Pred. No. 49;
2; Mismatches
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condition. The method comprises comparing the transcriptome/proteome of a competition of the composition of the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a condition specialised cell type, under two experimental conditions, and conditions are useful types under experimental conditions. ABV78116 specialised cell types under experimental conditions. ABV787873-ABV78116 conditions of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, appoposis, biological response to hypoxia conditions, or hypoxic-associated condition, such as patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
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                                         14-AUG-2001;
01-NOV-2001;
26-NOV-2001;
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                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                       spinal
                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                 Human Protein P05455,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 35; Page 425; 538pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially
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                                                                                                                                                                                                                        nerve
                                                                                                                                                                                                                                    pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction injury; CCI;
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                                         2001US-0312147P.
2001US-0346382P.
2001US-0333347P.
                                                                                                     2002WO-US025765
                                                                                                                                                                                                                      injury;
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55.6%;
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Pred. No. 49
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(GEHO) (FARB)

GEN HOSPITAL BAYER AG.

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RESULT 7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18
                                                                                    longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                          5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 5' EST;
gene therapy; 
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                                                         Sequence 92
                                                                                                                                                                                                                                                        The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
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                                                                                                                                                                                                                                                                                                                                   diagnostic,
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Local Similarity nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
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            48.3%;
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66.7%;
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Pred. No. 1.1;
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Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus antibacterial;
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                        25-MAR-2003
12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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08-NOV-1997;
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                                                                                                                                                    AAW03716 standard;
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gene therapy
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97US-0064964P.
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28-SEP-1999;
29-SEP-1999;
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                                                                                                                                                                                                                        Drosophila melanogaster.
                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling;
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05-OCT-1999;
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11-JUL-2000; 2000US-00614150.
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99US-0161361P.
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99US-0161404P.
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RESULT 6
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Best Local Similarity
Matches 8; Conserv
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                                                                                New compound containing acidic and aromatic amino acids, antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La
                                                                                                                                                                                                                                                                                                                                                                                                 Viral replication internal ribosome
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                                                       Claim 10; Page 16; 19pp; English.
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                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                                                                                                                                                                                                                                     agricultural;
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            ABG72119
                                                                                                                                                                        Sequence 390 AA;
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11-JUL-2000; 2000US-00614150
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           standard; peptide; 16
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Pred. No. 1.1;
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Pred. No. 4.6e-09;
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RESULT 4
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal ribosome viral life cycle;
                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                       AAG38952;
                                                                                                                                                                                                               AAG38952 standard; protein; 413 AA
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dasgupta A,
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                                                  Arabidopsis thaliana
                                                                             termination sequence
                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                            18-OCT-2000
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                                                                                                                                                                                                                                                                                                                                         l Similarity
                                                                                                                                                                                                                                                                                                           EASTIRQ-EYYFGD 17
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                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tion inhibitor; IRES initiated translation; LAP; some entry site initiated translation; La antigen protein; cle; antiviral therapy; pharmaceutical; veterinary; horticultural; virucide.
                                                                                                                                                                                                                                                                                                                                                    49.4%;
                                                                                                                                  protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baidya N
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Pred. No. 0.62;
L; Mismatches
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06-SEP-2000

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Minimum
Maximum
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Perfect score:
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Maximum Match
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                                                                                                                                                                                                                BB
                                                                                                                                                                                                                seq length: 0
seq length: 2000000000
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90
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first 45 summaries
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Compugen Ltd.
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score greater (is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	თ	4	ω	N	P	Result No.
43	43	43	43	43	43	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	43.5	44	44	4.	52.5	90	Score
47.8	47.8	47.8	•	47.8	47.8	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.3	48.9	48.9	49.4	58.3	100.0	Query Match
507	507	448	448	184	129	460	460	439	415	415	408	408	408	408	408	408	136	92	18	512	413	16	390	18	Length
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ABG93112	AAR42284	AAR40920	AAR41516	ABU54886	AAM84747	ABP41511	AAB58987	ABG08417	ADE63993	ADE63989	ADE62859	ADE63995	ADD46272	ADE63991	ABP65252	AAW03716	ABP40135	AAG01351	ABG72102	ABB57841	AAG38952	ABG72119	ABB65316	ABG72118	ID
Abg93112 S. cerevi	Pro	Aar40920 NHS-5 Pro	Aar41516 Cystathio	Abu54886 Metabolic	Aam84747 Human imm	Abp41511 Human ova	Aab58987 Breast an	Abg08417 Novel hum	Ade63993 Rat Prote	Rat	Ade62859 Human Pro	Ade63995 Human Pro	Add46272 Human Pro		Abp65252 Hypoxia-r		Abp40135 Staphyloc				Aag38952 Arabidops			18	Description

The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 18 AA;

New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.

Claim 1; Page 15; 19pp; English.

43 47.8 1252 4 AABO2008 43 47.8 1252 6 AABO29518 42.5 47.2 17 6 ABG72113 42.5 47.2 18 3 AAY52200 42.5 47.2 18 6 ABG72110 42.5 47.2 18 6 ABG72114 42 46.7 935 4 ABB627212 41 45.6 1035 4 ABB621323 41 45.6 1007 2 AAY19957 41 45.6 1036 2 AAY19956 41 45.6 1036 2 AAY1956	47.8 1252 6 47.8 1252 6 47.2 18 6 47.2 18 6 47.2 18 6 47.2 18 6 47.2 18 6 47.2 19 6 45.6 1031 3 45.6 1031 3 45.6 1036 3 45.6 1036 3 45.6 11036 3 45.	45	44	43	42	41	40	39	38	37	36	35	34	E E	32	31	30	29	28	27	Ċ
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	Aae02008 Aac29518 Abg72113 Abg72100 Abg72114 Abg72114 Abg72112 Abg62741 Abb62741 Abb62742 Abb62742 Aag51323 Aay19957 Aag51323 Aay19956 Abj676464 Abb6846464 Abb68464646464646464646464646464646464646	ABU01543	ADA36743	ABB64852	ABP70526	AAG51321	ABU19108	AAY19956	AAG51322	AAY19957	AAG51323	ABB62742	ABG72116	ABG72114	ABG72101	ABG72109	AAY52200	ABG72113	AA029518	AAE02008	

ALIGNMENTS

RESULT 1 ABG72118

Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide; mosquito. 16-APR-2001; 2001US-00836073. 24-OCT-2002. Culicoidea. Viral replication inhibiting peptide, MOSQUITO 28-JAN-2003 ABG72118; ABG72118 standard; peptide; WPI; 2003-058634/05. Dasgupta A, 12-APR-2002; 2002WO-US011589. WO200283858-A2 (UYCA-) UNIV CALIFORNIA OFFICE Das S, (first Baidya N; 18 PRESIDENT.

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TOPOLOGY: Innear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-1818-215
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US-09-721-456-215
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Patent No. 6617110
GENERAL INFORMATION:
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TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-No. 6617110-2000

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
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STRANDEDNESS: <Unknown>
                                                                                                                                                 APPLICATION NUMBER: US 08/851,843
FILLING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILLING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILLING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 38 amino acids
                                                                APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                            APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                    APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
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Nakamura, Toru
Chapman, Karen B.
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PCT/US97/17885
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                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
                                    7 ICHQIEEYYFGD 18
ICEQI-EYYFGD 11
                                                                                                                                                                                                                                                  LENGTH: 38 amino acids TYPE: amino acid
                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
                                                                          Conservative
                                                                      46.6%; Score 48.5; DB 4; Length 38; 83.3%; Pred. No. 0.38; tive 0; Mismatches 1; Indels
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Search completed: September 10, 2004, 18:05:10 Job time : 16.771 secs

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US-09-430-323-25
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Best Local (
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                        APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
TOPOLOGY: not relevant
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                              APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
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                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09430323
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Nakamura, 10.
Nakamura, Karen B.
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Harley, Calvin
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US-09-402-181B-215
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GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                               APPLICATION NUMBER: US 08/954,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO 07/US97/17885
FILING DATE: 01-CCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-CCT-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/724,643
FILLING DATE: 01-0CT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/402,181B FILING DATE: 29-Sep-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
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                                                                 NAME: Ausenhus,
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83.3%;
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Pred. No. 0.
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RESULT 11
US-08-974-549A-215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: 18 APR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 25-APR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/974,549A FILING DATE: 19-NOV-1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
                                 APPLICATION NUMBER: US 0 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                           APPLICATION NUMBER: 1
FILING DATE: 09-MAY-:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERMANE. PATENTIA PL-DOS #100
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                                                                                                                                                                                                                                                                 FILING DATE: 06-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                     FILING DATE: 14-AUG-1997
LIOR APPLICATION DATA:
APPLICATION NIMBER
                                                                                                                                                                                       APPLICATION NUMBER:
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Local Similarity 83.3%;
es 10; Conservative
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Harley, Calvin B.
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Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER: US 08/844,419
18-APR-1997
                                                                                                                                                                                                                                                                                                                                            TUMBER: US 08/846,017
25-APR-1997
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09-MAY-1997
                                                                                                                                                                     UMBER: US 08/911,312
14-AUG-1997
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06-MAY-1997
MBER: WO PCT/US97/17618
01-OCT-1997
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; MOLECULE TYPE: peptide
US-08-974-549A-215
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Patent No. 62011
Patent INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION UNMERR: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Te
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: Andrews, William H.
[TLE OF INVENTION: No. 6261836el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Apple, Randolph REGISTRATION NUMBER:
                 APPLICATION NUMBER:
                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Two Embarcadero Center, 8th Floor
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Nakamura, Toru
Chapman, Karen B.
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Harley, Calvin
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25-APR-1997
N. F. T.
                                                                18-APR-1997
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01-OCT-1996
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                                                                                 US 08/844,419
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               US 08/724,643
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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US-09-721-456-214
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GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION AUMBER: US/08/974,549A
PRICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                       FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                            APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
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                                                                                                       APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                             FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/846,017
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PONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                             LING DATE: 14-AUG-1997
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Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                             US 08/851,843
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                         015389-002610US
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Best Local
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GEORGE CECH, Thomas
TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
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INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
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FILING DATE: 06-MAY-
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TOTAL REPORT OF THE PROPERTY OF THE PROPE
                                                                                            NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 214:
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11; Conservative
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ii Harley, Calvin
hadrews, William H.
INVENTION: No. 6093809el Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lingner, Joachim
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18-APR-1997
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06-MAY-1997
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84.6%;
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                                                                                                                                                                                                       36,429
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Pred. No. 0.013;
                                                                                                                                                                                  015389-002930US
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US-08-974-549A-214
TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                   REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                             ARFULCATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: ADDIA 9-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                               FILING DATE: 01-OCT-1997 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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CLASSIFICATION:
                                                                                                     NAME: Apple, Randolph
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
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                                                  TELEPHONE:
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5. 6166178
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INVENTION: Human Telomerase Catalytic Subunit
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Two Embarcadero Center, Eighth Floor
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Chapman, Karen B.
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                                                      (415)
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06-MAY-1997
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25-APR-1997
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14-AUG-1997
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                                 576-0300
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                                                      576-0200
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Best Local Similarity
Matches 11; Conserv
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GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 214
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/402,181B
                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                               FILING DATE: 01-OCT-19
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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Harley, Calvin B.
Handrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                           REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
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CITY: San Francisco
                                    TELEFAX: (415)
                                                                                                                            NAME: Ausenhus, Scott
                                                                                                                                                                                                        APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                    TELEPHONE:
                                                                                                                                                                   APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997
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                                                                                                                                                                                                                                                                                                                   PLICATION NUMBER: US 08/854,050
LING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                      PLICATION NUMBER: US 08/851,843
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PLICATION NTARTY
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                                                    (415) 576-0200
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                                    576-0300
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Pred. No. 0
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ENGTH: 38 amino acids

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Best Local Similarity
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Query Match
Best Local Similarity
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APPLICANT: Cech,
                                                                                                                                                           TELEFAX: (415) 576-0300 (NFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                              NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-MAY-
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
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STATE: California
                                                                                                        STRANDEDNESS:
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FILING DATE: 06-MAY-1997
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                                                                                       TOPOLOGY:
                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                          ENGTH:
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amino acid
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Two Embarcadero Center, 8th Floor
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                         not relevant
                                                                                                                                                                                                                       (415) 576-0200
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                                                                                                          not relevant
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84.6%;
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Pred. No.
 Score 58; DB 3; Pred. No. 0.011;
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                  Length 37;
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US-09-430-323-24
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                                                                                               Matches
                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/854,050
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/846,017
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHITE Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                 TOPOLOGY: not relevant MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ II
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
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                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 ICHQIEEYYFGDF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICHO--EYYFGDF 11
                        ICHQ--EYYFGDF 11
                                                           ICHQIEEYYFGDF 19
                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/430,323 FILING DATE: 29-Oct-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                               LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09430323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                               Conservative
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Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ingner, Joachim
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                                                                                                                55.8%;
84.6%;
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                                                                                                                                                                                       SEQ ID NO: 24:
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                                                                                               0;
                                                                                           Score 58; DB 4; Length 37; Pred. No. 0.011; 0; Mismatches 0; Indels
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley
                                                             TELEPAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-1
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-1
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
                                                                                                                                                                                                                                                                                                                                                                                                          SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METH
                                                                                                                                                                                                         FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             FILING DATE: January 31, 1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/472,94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (404)-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                             NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: Januar
                                                                                                                                                                                                                                                                                                                             FILING DATE: AF CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: June 7 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2800 One Atlantic Center, 1250 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                              07/648,205
                                                                                                                                                                                                                                               07/472,947
                                                                                                                                                                              31,284
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Best Local Similarity
Thes 12; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                            REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 01-OCT-:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US
                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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MOLECULE TYPE:
                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Andrews, William H.
ITLE OF INVENTION: No. 6093809el Telomerase
JMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                          NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: CCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                        TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                 CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                 COPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cech, Thomas R.
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                               not relevant
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92.3%;
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Pred. No. 0.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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42.5
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length: 2000000000
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Gapop 10.0 ,
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| cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
| cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
| cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
| cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
| cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
| cgn2_6/ptodata/2/iaa/backfiles1.pep:*
   AALEAKICHQIEEYYFGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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              US-09-316-630-3
US-09-316-630-4
US-08-475-955-20
US-08-851-843A-24
US-08-854-050-24
US-09-402-181B-214
US-09-402-181B-214
US-09-402-181B-215
US-08-974-549A-215
US-08-974-549A-215
US-08-974-549A-215
US-08-974-549A-215
US-08-974-549A-215
US-09-430-23-25
US-09-431-517F-6
US-08-431-517F-6
US-08-431-517F-6
US-08-431-517F-5
US-09-107-532A-4729
US-09-107-532A-4729
US-09-107-332-872A-23
US-09-323-872A-23
US-09-323-872A-23
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Compugen Ltd
Sequence 3, Appli
Sequence 24, Appli
Sequence 24, Appl
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Sequence 214, Appl
Sequence 214, App
Sequence 214, App
Sequence 215, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 27, Appli
Sequence 4, Appli
Sequence 27, Appli
Sequence 28, Appli
Sequence 27, Appli
Sequence 28, Appli
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45	44	43	42	41	40	39	38.	37	36	3 5	34	33	32	31	30	29	28
39	39	39	40	40	40	40	40	40	40	40	41	41	41	41	41.5	42	42
37.5	37.5	37.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	38.5	39.4	39.4	39.4	39.4	39.9	40.4	40.4
122	99	86	1253	1253	263	255	214	203	102	41	497	410	307	289	463	699	611
4	4.	4.	ω	Н	N	4	4.	4.	4	4	4	4	4	4	4	4	4
US-09-732-210-62	US-09-543-681A-6663	US-09-300-008B-55	US-08-466-277-3	US-07-920-281C-3	US-08-864-799-1	US-09-107-532A-6662	US-09-205-258-965	US-09-328-352-7692	US-09-198-452A-56	US-09-205-258-970	US-09-489-039A-8926	US-09-543-681A-5407	US-09-328-352-5689	US-09-543-681A-8235	US-09-543-681A-6745	US-09-543-681A-5118	US-09-543-681A-5447
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
62, App1		55, App1	-	3, Appli	1, Appli	6662, Ap	965, App		56, Appi		8926, Ap	5407, AD	5689, AD	8235, AD	6745, AD	5118, AD	5447, Ap

ALIGNMENT

US-09-316-630-3

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IR:
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CR.
FILE REFERENCE: 22000-20548.21
FULR REPELICATION NUMBER: US/09/316,630
CURRENT APPLICATION NUMBER: 08/817,953
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1997-10-06
                                                                                                                                                                                                                                             US-09-316-630-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-316-630-3
                                                             Sequence 4, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERPERENCE WITH VIRAL
TITLE OF INVENTION: SMALL YEAST RNA REVEALS
FILE REFERENCE: 22000-20548.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1994-10
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-05
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09316630 Patent No. 6291637 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
CURRENT APPLICATION NUMBER: US/09/316,630 CURRENT FILING DATE: 1999-05-21 PRIOR APPLICATION NUMBER: 08/817,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                       1 AALEAKICHQIEEYYFGDF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                   AALEAKICHQI-EYYFGDF
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1994-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                           85.1%;
94.7%;
                                                                                                                                                                                                                      US/09316630
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 88.5; DB 3;
Pred. No. 5.6e-08;
0; Mismatches (
                                                                                          IRES-MEDIATED TRANSLATION BY A CRITICAL RNA-PROTEIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRES-MEDIATED TRANSLATION BY A CRITICAL RNA-PROTEIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
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N-PSDB; AAS72604.

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RESULT 15
AAB58987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc sequences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cc in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal carrivity of (II) or to treat disease states involving (II). (II) is constituted in tissue, as molecular weight markers and as a food conjupeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging cof sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The collective and polymucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cc polypeptide and polymucleotide sequences have application of mutations cc amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic camino acid sequences of the invention. Note: The sequence data for this captant did not appear in the printed specification, but was obtained in cc electronic format directly from MIPO at for sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                  Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antivaliergic; hepatotropic; antidiabetic; antiinflammatory; antivicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                   08-MAR-2000;
                                                                                                                                                                                                                                                                         WO200055173-A1
                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breast and ovarian cancer associated antigen protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB58987 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 38776; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                               12-MAR-1999;
                                                                                                                                                                                                      21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
   (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                                                   2000WO-US005881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
GENOME SCI INC
                                                               99US-0124270P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 460 AA
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94.7%;
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Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
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Search completed: September 10, Job time: 60.5413 secs

2004, 17:51:50

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                                                                                    Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                     or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antivicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune the production and treatment of immatorial autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhumatoria arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention as sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agoning the protein and characterisation of the DNA and protein associated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1149-11150; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                     infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological diseases.
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  63
l Similarity
                                                                                                                                                                          460 AA;
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                                                                                        Conservative
                                                                                                        85.1%;
94.7%;
                                                                                        <u>.</u>
                                                                                      Score 88.5; DB 3;
Pred. No. 1.4e-05;
0; Mismatches 0;
                                                                                        0
                                                                                                                               Length 460;
                                                                                        Indels
                                                                                        1;
                                                                                        Gaps
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

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                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                               14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
         WPI; 2003-268312/26
GENBANK; P38656.
                                                                                                                                                                                            Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                          Rat Protein
                                  Woolf C,
                                                                                                                     14-AUG-2002; 2002WO-US025765
                                                                                                                                        27-FEB-2003
                                                                                                                                                          WO2003016475-A2
                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                          29-JAN-2004
                                                                                                                                                                                                                                                                              ADE63993 standard; protein; 415 AA.
                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                              1 AALEAKICHQIEEYYFGDF 19
                                                      GEN HOSPITAL BAYER AG.
                                                                                                                                                                                                                                                                                                                             AALEAKICHQI-EYYFGDF 28
                                   D'urso D,
                                                                                                                                                                                                                         P38656,
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                         SEQ ID NO 9939.
                                                               CORP
                                   Befort K,
                                   Costigan M;
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CC derivative or allelic variation of the nucleic acid sequence. Also comprising the vector comprising the nucleic acid sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying a nucleotide sequence cc which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cc subjected to pain, a method for identifying an agent the expressed in neuronal tissue of a first animal compound that regulates the compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound or small molecule that regulates the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a cc invity in an animal of one or more of the polypetides given in the specification, a method for identifying a compound useful in treating capain and a pharmaceutical composition composition the one or more compound useful in treating compositions and aparmaceutical composition composition composition the one or more compound useful in treating capain (e.g. spinal segmental nerve injury (Chung), chronic constriction constriction (e.g. spinal segmental nerve injury (Chung), chronic constriction constriction will be sequence presented is a rat protein (shown in Table 2 of the specification, which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed constriction is pacification, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at the printed constriction 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
                                                                    ftp.wipo.int/pub/published_pct_sequences.
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Query Match Best Local S Matches 18

Similarity

85.1%; 94.7%;

Score 88.5; DB 7; Pred. No. 1.3e-05; Mismatches

Length 415; Indels

Conservative

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0

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Gaps

۳.

Sequence 415

AΑ;

Sequence 415

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The sequence data for this patent did not form part of the psecification, but was obtained in electronic form directly

expressed during pain. Note: form part of the printed

WIPO at

ftp.wipo.int/pub/published_pct_sequences.

that is differentially expressed in neuronal tissue of a first animal consumers of the pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating composition and a pharmaceutical composition comprising the one or more colored to their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating conjunction (e.g. spinal segmental nerve injury (Chung), chronic constriction conjunction (c.g. spinal segmence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence.

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Query Match
Best Local (
                                       Matches
11
                                       18;
                  1 AALEAKICHQIEEYYFGDF 19
                                                  Similarity
 AALEAKICHQI-EYYFGDF
                                       Conservative
                                                  85.1%;
94.7%;
                                       0;
                                                  Score 88.5; DB 7;
Pred. No. 1.3e-05;
                                        Mismatches
                                                           7;
                                        0
                                                           Length 415;
                                         Indels
                                         1:
                                        Gaps
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Human; chromosome mapping; gene mapping; gene therapy;
food supplement; medical imaging; diagnostic; genetic c
                                                                                                                           Novel human diagnostic protein #8408
                                                                                                                                        13-FEB-2002 (first entry)
                                                                                                                                                                ABG08417 standard; protein;
                                                                                                                                                    ABG08417;
                                                                                                                                                                  439
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forensic;

31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167

HYSEQ INC.

30-MAR-2001; 2001WO-US008631

WPI; 2001-639362/73

Drmanac RT,

Liu C,

Tang YT;

11-OCT-2001.

WO200175067-A2 Homo sapiens

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RESULT 11
ADE62859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragmu derivative or allelic variation of the nucleic acid sequence. Also
                                                                   Claim 1; Page; 1017pp; English
                                                                                                   New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                       GENBANK;
                                                                                                                                                                        WPI; 2003-268312/26.
                                                                                                                                                                                                        Woolf C,
                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein P05455, SEQ ID NO 8793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE62859 standard; protein; 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electr
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002; 2002WO-US025765
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                                                                                                                                                        P05455.
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94.7%;
                                                                                                                                                                                                        Befort K,
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Pred. No. 1.3e-05;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates CC the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a CC method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the CC specification, a method for identifying a compound useful in treating CC polypeptides or their antibodies. The polynucleotide or the compound that completion or the polypeptides or the compound that comparison to the polypeptides or their antibodies. The polynucleotide or the compound that comparison is differentially expressed during pain. Note: the specification which is differentially expressed during pain. Note: the specification which is differentially expressed during pain. Note: the specification which is differentially expressed by the printed during pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                              14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat Protein P38656, SEQ ID NO 9935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004 (first entry)
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                                                                                                      WPI; 2003-268312/26.
                                                                                                                                        Woolf C,
                                                                                                                                                                            (GEHO )
(FARB )
                                                                                                                                                                                                                                                                                                       14-AUG-2002;
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                                                                                                                                                                            GEN HOSPITAL
BAYER AG.
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                                                                                                                                      D'urso D,
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                                                                                                                                                                                                                                                                                                       2002WO-US025765.
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94.7%;
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Pred. No. 1.3e-05;
                                                                                                                                        Costigan
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New composition comprising two or more isolated polypeptides, preparing a medicament for treating pain in an animal.

useful

for

P38656

Claim 1; Page; 1017pp; English

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RESULT 9
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                        The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a expressed in an animal subjected to pain, a method for identifying a
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(FARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Protein P05455,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 1017pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2002; 2002WO-US025765
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Pred. No. 1.3e-05;
0; Mismatches 0;
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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic cons
                                                                                                                                                        Claim 1; Page; 1017pp; English.
                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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                                                                                                                     invention discloses a composition comprising two or more isolated rat
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No. 1.3e-05;
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Matches 1
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                                                                                     The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under specialised conditions. ABV7873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating hypoxia-regulated patient, for manufacture of a medicament for treating hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-2002
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pathology
                           conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions, comprises comparing the types under different conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000; 2000GB-00030076.
08-FEB-2001; 2001GB-00003156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-2001; 2001WO-GB005458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200246465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP65252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-627238/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Page 425; 538pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AALEAKICHQI-EYYFGDF 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mundy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
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94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>.
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krige D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingsman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isolated from a human liver
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Best Local
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01-NOV-2001;
26-NOV-2001;
        claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for monitoring the therapeutic treatment of a disease or physiologic condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflamm conditions, wound healing, inflammation, erythropoiesis or hair loss
                                                                                                                                                                                                                                    The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                 New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                               Woolf C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Protein P05455,
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                                                                                                                                                                                                                                                                                                                                                                                  GENBANK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEHO )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pain; neuronal segmental nerve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEN HOSPITAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0312147P.
2001US-0346382P.
2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal tissue; gene therapy;
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 9937.
                                                                                                                                                                                                                                                                                                                                 two or more isolated polypeptides, useful treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408
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Pred. No. 1.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5;
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                                                                                                                                                                                                                                                      fragment,
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dasgupta A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2001; 2001US-00836073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal ribosome entry site initiated translation; La antigen protein;
viral life cycle; antiviral therapy; pharmaceutical; veterinary;
agricultural; horticultural; virucide; bovine.
                                                                                                                                                                                                     Human; 5' EST; expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 6; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT
                                                                                                                                                                                      gene therapy;
  Dumas Milne Edwards J,
                                                                                                                                   EP1033401-A2
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                       06-OCT-2000
                                                                                                                                                                                                                                                                                                          AAG01351 standard; protein; 92 AA
                                                     26-FEB-1999;
                                                                               21-FEB-2000; 2000EP-00200610
                                                                                                         06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Das S,
                                                                                                                                                                                       chromosome mapping.
                                                                                                                                                                                                                             protein,
                                                      99US-0122487P
                                                                                                                                                                                                                                                                                                                                                                                                                                           85.1%;
    Duclert A,
                                                                                                                                                                                                                             SEQ ID NO:
                                                                                                                                                                                                   sequence tag; secreted protein; cDNA isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 88.5; DB 6;
Pred. No. 4.3e-07;
0; Mismatches 0;
                                                                                                                                                                                                                               5432.
    Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
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RESULT 6
AAW03716
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma overlap syndrome - useful for diagnosis and treatment of autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
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N-PSDB; AAC01357.
                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW03716 standard;
                                                                                                                                                                                                                                            27-MAY-1987;
                                                                                                                                                                                                                                                                       30-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                          systemic
                                                                                                                                                                                                                                                                                                                                                                                                 Human autoantigen La(SS-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW03716;
                                                                                                                            WPI; 1996-362015/36
                                                                                                                                                        Keene
                                                                                                                                                                                                                31-DEC-1984;
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        Autoimmune
                                                                                                                                                                                    (UYDU-) UNIV
                                                                                                                                                                                                                                                                                                   US5541291-A.
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                                                                                                                                                                                                                                                                                                                                                        ne disease; La autoantigen; Sjogren's lupus erythematosus; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence is a polypeptide encoded by one of a large number of ived from mRNAs encoding secreted proteins. The 5' ESTs were
                                          5
                                                                                                                                                                                     DUKE.
                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                84US-00687908
                                                                                                                                                                                                                                            87US-00054871
                                          15-16; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.1%;
94.7%;
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No. 2.5e-06;
                                                                                                                                                                                                                                                                                                                                                                        syndrome;
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The human lupus antigen (La) is diagnostic for Sjogren's syndrome, well as occurring in systemic lupus erthematosus patients. The La

protein

Disclosure;

닭 S

Length 19;

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                                                                                                                                      CC This sequence is the La autoantigen binding domain (LAP). LAP is a CC cellular protein which binds to an internal ribosome entry site (IRES). CC The peptide is used to inhibit mRNA translation, viral protein CC translation or viral replication. Viral mRNA translation is initiated at the IRES and the LAP peptide prevents translation initiation factors from CC binding at the site. The peptide can be used alone or in combination with CC an inhibitor RNA (IRNA see AZ45200). The LAP peptide is useful as an CC especially viral mRNA. Examples of viruses which can be inhibited are CC picornavirus, flavivirus, coronavirus, hepatitis AB or C viruses, rinovirus, cromavirus, adenovirus, and parainfluenza virus, poliovirus, rinovirus, CC rinbidovirus, encephalomyocarditis virus, foot-and-mouth disease CC virus, echo virus, hepatitis virus, The peptide CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide CC also inhibits replication of the above viruses. The LAP peptide consider to the host call
                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        La autoantigen; LAP; internal ribosome entry site; IRES; translation; viral replication; IRNA; antiviral agent, piccornavirus; flavivirus; coronavirus; hepatitis virus; habdovirus; adenovirus; coxsackie virus; parainfluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus; foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
                                                                                               Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New yeast inhibitory peptide useful for inhibiting viral protein translation and replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-062712/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Das S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                               Local
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                                l Similarity
18; Conserv
 1 AALEAKICHQIEEYYFGDF 19
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                                                                                                                                                                                                                                                                                                                                                                                                                              Page 57;
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                                Conservative
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                                                                                                                               host
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                                                                                                                                                                                                                                                                                                                                                                                                                            81pp; English.
                                                                                                                               cell
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94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus
                             Score 88.5; DB 3;
Pred. No. 4.3e-07;
0; Mismatches 0;
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Pred. No. 1.5e-09;
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                                                             Length 18;
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                                                                                                                                                                                                                            Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                      The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen p viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide.
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                      Viral replication inhibiting peptide, BOVINE.
                                                    28-JAN-2003
                                                                                                      ABG72114 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-058634/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dasgupta A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2001; 2001US-00836073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral replication
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                                                                                                                                                                                                                                                                                                             ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCA-) UNIV CALIFORNIA OFFICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2002; 2002WO-US011589
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                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                             AALEAKICHQIEEYYFGDF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AA;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Das S,
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                                                  (first entry)
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94.7%;
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                                                                                                                                                                                                                                          Score 88.5; DB 6;
Pred. No. 4.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRESIDENT
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                                                                                                                                                                                                                                                        Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               La antigen protein;
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Viral replication inhibitor; IRES initiated translation; LAP;

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-836-073-16
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               September 10, 2004, 16:58:20;
                                                                                                                               A_Geneseq_29Jan04:*
1: geneseqp1980s:*
                                                                                                                                                                                                                                                                                                                                                     1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AALEAKICHQIEEYYFGDF 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                         geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
                     geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 ; Search time 59.4413 Seconds
(without alignments)
90.314 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                      1586107
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	ហ	4	ω	N	ш	No.	Result
75.5	76.5	76.5	76.5	79.5	80.5		83.5	84.5	.88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5	88.5		88.5		88.5		104	Score	
72.6	73.6	٠	73.6	76.4	77.4			81.2		85.1	85.1			85.1	85.1	85.1	85.1	85.1	85.1	85.1	•		85.1	100.0	Match Length	Query
L	18	18	18	18	18	18	18	17	460	460	439	415	415	408	408	408	408	408	408	92	18	18	18	19		
σ	0	σ	δ	σ	σ	σ	σ	σ	ហ	ω	4	7	7	7	7	7	7	w	N	ω	9	σ	w	6	BB	
ABG72108	ABG72104	ABG72103	ABG72102	ABG72110	ABG72112	ABG72109	ABG72111	ABG72113	ABP41511	AAB58987	ABG08417	ADE63993	ADE63989	ADE62859	ADE63995	ADD46272	ADE63991	ABP65252	AAW03716	AAG01351	ABG72114	ABG72101	AAY52200	ABG72116	ID	
dei rein sorz/fow	Viral	-	-	Viral		9	μ	W	-	~		Rat Pr	Rat	Huma	Ade63995 Human Pro	Add46272 Human Pro	Ade63991 Human Pro	Abp65252 Hypoxia-r	Aaw03716 Human aut	Aag01351 Human sec	Abg72114 Viral rep	•	Aay52200 Human La	Abg72116 Viral rep	Description	

45	44	43	42	41	40	ب و	38	37	36	35	34	33	32	31	30	29	28	27	26
45.5	45.5	45.5	45.5	45.5	45.5	45.5	46	46.5	47	47	47	47	47	49	62.5	63	64.5	65.5	73.5
43.8	43.8	43.8	43.8	43.8	43.8	43.8	44.2	44.7	45.2	45.2	45.2	45.2	45.2	47.1	60.1	60.6	62.0	63.0	70.7
2047	863	675	643	643	425	132	352	16	482	482	482	482	456	2169	21	18	18	18	18
4	7	6	7	4	4	ω	σ	6	N	Ŋ	N	N	N	4	2	σ	6	σ	Q
AAB99541	ADC31112	ABR43633	ADC21971	AAB99540	AAM25631	AAB51905	ABR53809	ABG72119	AAW78355	AAW40813	AAR53461	AAR41659	AAW41695	AAG91701	AAR43394	ABG72106	ABG72105	ABG72115	ABG72107
Aab99541	Adc31112	Abr43633	Adc21971	Aab99540	Aam25631	Aab51905	Abr53809	Abg72119	Aaw78355				Aaw41695	Aaggiroi	Aar43394	ADG/2106	ADG / ZIUS	Abg/2115	Abg72107
Human CLA	Human nov			Prelimin	Human pro	Human sec	Procein 8	Viral rep	Rabbit	Rabbic	Tapine I	Fabine 5	Kappic I	C grucan	La/SSD ep	virai rep		viral rep	

ALIGNMENTS

RESULT 1 ABG72116

Ħ	ABG72116 standard; peptide; 19 AA.
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AC	ABG72116;
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DI	28-JAN-2003 (first entry)
X	
H	Viral replication inhibiting peptide, RAT.
Ž	
Š	Viral replication inhibitor; IRES initiated translation; LAP;
Ş	internal ribosome entry site initiated translation; La antigen protein;
Ş	<pre>viral life cycle; antiviral therapy; pharmaceutical; veterinary;</pre>
Ş	agricultural; horticultural; virucide; rat.
×,	
80	Rattus sp.
X	
PN	WO200283858-A2.
X	
PD	24-OCT-2002.
×	
ЭF	12-APR-2002; 2002WO-US011589.
X	
3	16-3001. 2001ITG-00836073

16-APR-2001; 2001US-00836073.

(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

Dasgupta A, Das S, Baidya N;

WPI; 2003-058634/05.

New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.

Claim 1; Page 15; 19pp; English.

The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blockemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 19 AA;

the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating

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RESULT 15
ABG08417
ID ABG08
XX ABG08
XX ABG08
XX ABG08
XX Human
XW Hood
XX Homo
XX Hom
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The invention relates to isolated polynucleotide (I) and polypeptide (II) seequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal
                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 38776; 103pp; English.
                                                                                                                                                                                                                                                                                                                                          biodiversity.
                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac
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23-AUG-2000;
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DB; AAS72604.
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13 LEAKICHQIEYYFGDF 28
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Similarity 81.2%;
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2000US-00649167.
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Pred. No. 0.0022;
1; Mismatches
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Best Local (
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                                                                                                                                                                                                                                                              Sequence 439 AA;
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3 LDTKICEQIEYYFGDF 18
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           The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; P38656.
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a method for producing a pharmaceutical

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENBANK; P38656.
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(FARB )
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                                                                                 derivative or allelic variation of the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for pain, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that composition is useful for preparing a medicament for treating componal is a sectivity is useful for preparing a medicament for treating componal is a method for identifying a compound that the componal that the componal regeneral in a merce into the componant for treating componer or the componant for treating componer or the compo
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01-NOV-2001;
26-NOV-2001;
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page; 1017pp;
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BAYER AG.
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The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an array, a method for identifying a compound that regulates the cativity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating cativity animand a pharmaceutical composition comprising the one or more
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                                                                                                                                                                                                                                                                                                                                       New composition comprising preparing a medicament for
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; 2001US-0346382P.
; 2001US-0333347P.
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Pred. No. 0.0022;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                         more isolated polypeptides, ng pain in an animal.
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RESULT 9
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                                                                                                         CC subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a combound or small molecule that regulates the cativity in an animal of one or more of the polypeptides given in the greatification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more complypeptides or their antibodies. The polymucleotide or the compound that compute the sequence presented for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene conjury (SNI)) in an
Query Match
Best Local Similarity 81.3
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                         Sequence
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                                                                                                              408 AA;
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  Score 76; DB 7; Le
Pred. No. 0.0022;
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, contrivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating capacitic and a pharmaceutical composition comprising the one or more computed that regulates the specification, a method for identifying a compound useful in treating capain (e.g. spinal segmental nerve injury (chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene constriction the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed constrained in electronic form of the print
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic cons spared nerve injury; SNI; Chung.
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                  specification, but was obtained
ftp.wipo.int/pub/published_pct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                           Sequence 408 AA;
                                                                                                                                     cellular ribonucleoprotein particle; most La patients contain some Ro antibodies and vice versa. La cDNA has been isolated from a human liver library. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                          The human lupus antigen (La) is diagnostic for Sjogren's syndrome, as well as occurring in systemic lupus erthematosus patients. The La protein is clinically related to the Ro protein that is highly common among autoimmune patients. La and Ro antigens sometimes reside on the same
                                                                                                                                                                                                                                                                                        overlap syndrome - useful for diagnosis
                                                                                                                                                                                                                                                                                                      Auto-antigen U2-RNP, associated with severe
                                                                                                                                                                                                                                                                                                                                  WPI; 1996-362015/36.
                                                                                                                                                                                                                                                                                                                                                             Keene JD;
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12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autoimmune disease;
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(first entry)
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erythematosus; diagnosis.
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RESULT, 8
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                                                                                                                                                 The present invention relates to methods for identifying genes and corrections that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a condition general seed cell type, under two experimental conditions, and conditions are cell type, under two experimental conditions, and conditions are cell types under sexperimental conditions. ABV7873-ABV78116 and ABP55061-ABP55257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating hypoxia-regulated conditions, and for regulating tumourigenesis, and conditions, and for regulating tumourigenesis, and proteins are useful for treating hypoxia-regulated conditions, and for regulating tumourigenesis, appicosis, biological response to hypoxia conditions, or hypoxic-associated conditions, such as cancer, ischaemic conditions, reperfusion injury, conditions, wound healing, inflammation, erythropoiesis or hair loss
   Query Match
Best Local :
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08-FEB-2001;
25-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine hypoxia; tumourigenesis; anglogenesis; apoptosis; cancer; hypoxia; tumourigenesis; anglogenesis; apoptosis; cancer; isthaemic condition; reperfusion injury; retinopathy; neonatal stress preeclapmsia; atherosclerosis; inflammatory condition; wound healing;
                                                                                             Sequence 408
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inflammation;
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2001GB-00003156.
2001GB-00025666.
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76.0%;
81.2%;
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   Score 76; DB 5;
Pred. No. 0.0022;
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                                Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
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                                                                                                                                                                     Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18
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(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
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RESULT 6
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) is obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping processing the contract of the contr
                                                                                                                                                                                                                                         Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
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DB; AAC01357.
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Pred. No.
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7e-05;
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AAY52200;
                                               AAY52200 standard;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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agricultural; horticultural; virucide; mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the La autoantigen binding domain (LAP). LAP is a CC cellular protein which binds to an internal ribosome entry site (IRES). CC The peptide is used to inhibit mRNA translation, viral protein CC translation or viral replication. Viral mRNA translation is initiated at the IRES and the LAP peptide prevents translation initiation factors from thinding at the site. The peptide can be used alone or in combination with CC an inhibitor RNA (IRNA see ARA5200). The LAP peptide is useful as an CC antiviral agent, which works through the inhibition of mRNA translation, cespecially viral mRNA. Examples of viruses which can be inhibited are CC picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses, rhabdovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus, corosackie virus, encephalomyocarditis virus, foot-and-mouth disease CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck and human hepatitis B virus, and vesticular stomatitis virus. The peptide calso inhibits replication of the above viruses. The LAP peptide not cover the cover of the cove
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Best Local S
Matches 13
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                                                                                         28-JAN-2003
                                                                                                                                                                              ABG72101 standard; peptide; 18
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Viral replication inhibitor; IRES initiated translation;

Viral

replication inhibiting

peptide, LAP.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Abg72116 Viral rep Abg72103 Viral rep	Viral Viral	Viral	Abg72102 Viral rep Abg72104 Viral rep	1 Human c	Abg0841/ Nover num Aab58987 Breast an	Rat P	Rat	Ade62859 Human Pro	Ade63995 Human Pro	Add46272 Human Pro		Abp65252 Hypoxia-r	Aaw03716 Human aut	Human	4 Viral		٥	Abg72113 Viral rep	Viral re	Description

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Abg72106	Abu18600	Aab43110	Abp43683	Aau96341	Aau96342	Aag47712	Aag47713	Aag47714	Abb65316	Abu43510	Abp70526	Abm/2091	Abjiede	Abg/2119	Abg72117	Abg72108	Abg/2107	Abg72105	Hattagar
Viral rep	Protein e	Human Oke	FLJ11196	Der HMW-m	Der HMW-m	Arabidops	Arabidops	Arabidops	Tradosoru	Protein e	Histone a	Scapnyroc	Pathogen	Viral rep		•	_		ř

ARBSULT 1 ARBO72115 ARBO72115 ARC ARBO7217 ARC ARBO72 ARBO Viral replication inhibitor; IRBS initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide; xenopus. Viral replication inhibiting peptide, XENOPUS ABG72115; Xenopus sp. 28-JAN-2003 ABG72115 standard; peptide; (first entry) 18 A

ALIGNMENTS

WO200283858-A2

24-OCT-2002.

12-APR-2002; 2002WO-US011589.

16-APR-2001; 2001US-00836073.

(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT

Dasgupta A, Das S, Baidya N;

WPI; 2003-058634/05.

New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.

Claim 1; Page 15; 19pp; English.

The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) inlitiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 18 AA; This Page Blank (uspto)

Search completed: September 10, 2004, 18:11:55 Job time : 40.424 secs

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APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, S.
APPLICANT: Baidya, Narayan
ITITLE OF INVENTION: MSTHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILLING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
INUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 19
TYPE: PRT
ORGANISM: Rat
US-09-836-073-16
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; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 10
; SEQ ID NO 10
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; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
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Patent No. US20020173475A1
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Best Local (
                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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Best Local Similarity
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                                                                                                                      APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-21
                                                                                                           NUMBER OF SEQ ID NOS: 19
                            LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
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Similarity 94.4%;
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94.7%;
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Pred. No. 2.8e-07;
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US-09-836-073-4
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; ORGANISM: Homo Sapiens
US-09-836-073-3
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APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                               Matches
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT EPPLICATION UNMEER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PELING DATE: 1999-05-21
NUMBER OF SEO ID NOS: 19
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                         EAKICHQIEYYFGDF 18
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Pred. No. 8.
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; Sequence 9, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgipta, Asim
; APPLICANT: Dasg. S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
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US-09-836-073-13
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SEQ ID NO 13
LENGTH: 17
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                        Query Match
Best Local Similarity
Matches 17; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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Patent No. US20020173475A1
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Best Local :
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PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
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ORGANISM: Homo sapiens
                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                 LENGTH: 18
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AALEAKICHQIEYYFGD 17
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                                                                Conservative
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                                                                              93.9%; Score 93; DB 9; I
100.0%; Pred. No. 9.3e-08;
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Pred. No.
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Pred. No. 2.8e-07;
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APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Dasidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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US-09-836-073-11
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US-09-836-073-12
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RESULT 11
US-09-836-073-10
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
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Patent No. US20020173475A1
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: WETHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
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ORGANISM: Homo Sapiens
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Local Similarity 94.4%;
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l Similarity 94.4%;
17; Conservative
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Pred. No. 1.
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; Sequence 10, Application US/09836073; Patent No. US20020173475A1; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT

TO INHIBIT VIRAL REPLICATION

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; ORGANISM: Bovine
US-09-836-073-14
                                                                                                                         US-09-925-298-695
                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-477
                                                                                                                                             RESULT 4
                Sequence 695, Application US/09925298
Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 477
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Best Local Similarity
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TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PELICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
CURRENT APPLICATION NUMBER: US/09/925,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ward,
APPLICANT: Mund
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                                                                                                                                                                                                                                                                                      Match 100.0%; Score 99; DB 12; Local Similarity 100.0%; Pred. No. 2.5e-07;
                                                                                                                                                                                              18; Conservative
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Rayner, William Nigel
Naylor, Stuart
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White, Jonathan
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b. US20030203372A1
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y, Christopher Robert
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US-10-264-049-2643
Sequence 2643, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
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APPLICANT: Birse et al.
FILE REFERENCE: PA133P1
CURRENT APPLICATION: NUMBER: US/10/264,049
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens US-10-102-806-695
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US-10-102-806-695
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US-09-925-298-695
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SEQ ID NO 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 695, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 695
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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TYPE: PRT
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b. US20030054421A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 99; DB 14; ilarity 100.0%; Pred. No. 2.8e-07; Conservative 0; Mismatches 0;
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SOFTWARE: PatentIn Ver. 3.1 SEQ ID NO 2643 LENGTH: 460

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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143.151 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	14	13	12	11	10	9	œ	7	თ	v	4	w	2	₽	Result No.
87	87	87	88.5	90	91	91	93	95	99	99	99	99	99	99	Score
87.9	87.9	87.9	89.4	90.9	91.9	91.9	93.9	96.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match I
18	18	18	19	18	18	18	18	17	460	460	460	408	18	18	Query Match Length DB
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US-09-836-073-4	US-09-836-073-3	US-09-836-073-2	US-09-836-073-16	US-09-836-073-10	US-09-836-073-12	US-09-836-073-11	US-09-836-073-9	US-09-836-073-13	US-10-264-049-2643	US-10-102-806-695	US-09-925-298-695	US-10-170-385-477	US-09-836-073-14	US-09-836-073-1	ID
Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 16, Appl	Sequence 10, Appl	Sequence 12, Appl	Sequence 11, Appl	Sequence 9, Appli	Sequence 13, Appl	Sequence 2643, Ap	Sequence 695, App		Sequence 477, App	Sequence 14, Appl	Sequence 1, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
48	48	48	48	50	50	50	52	53	57	8	58.5	œ	œ •	œ	æ	59	59	59	59	59	59	59	68	83	73	75	76	83	84
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12	10	9	9	14	12	12	16	16	9	14	14	14	10	ø	9	14	14	14	12	10	9	9	12	9	15	9			9
US-10-325-810-216	8-486-2	253-26	43-67	-177-478-	Ψ	0-424-599-2546	437-963-	US-10-437-963-125036	US-09-836-073-19	US-10-054-611-24	- 1	US-10-053-758-24	US-09-438-486-24	US-09-766-253-24	US-09-843-676-24	-10-054-	US-10-054-295-25	-10-053-758-2	310	US-09-438-486-25	US-09-766-253-25	43-676-2	US-10-325-810-214	US-09-836-073-6	\mapsto	US-09-836-073-5	US-09-836-073-15	Ÿ	US-09-836-073-7
Sequence 216, App	Sequence 26, Appl	26,		е в	25	O	Sequence 128072,	e 12	19	24	24, App	24,	Sequence 24, Appl		4	e 25,	Sequence 25, Appl	e 25,	Sequence 215, App	e 25,	, ,	Sequence 25, Appl	214	껕	Sequence 20, Appl		e 15,	e 8	-

ALIGNMENTS

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APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
ITITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOPTWARE: FastSEQ for Windows Version 4.0
ISEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANIZM: Homo Sapiens
                                                                                                  RESULT 2
US-09-836-073-14
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US-09-836-073-1
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                                    Sequence 14, Application US/09836073 Patent No. US20020173475A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 18; Conservative
APPLICANT: Dasgupta, APPLICANT: Das, S.
                                                                                                                                                                                     1 AALEAKICHQIEYYFGDF 18
                                                                                                                                                                                                            1 AALEAKICHQIEYYFGDF 18
                                                                                                                                                                                                                                                                                           100.0%; Score 99; DB 9; 100.0%; Pred. No. 1.1e-08;
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                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                            Length 18;
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PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

18-APR-1997

US 08/844,419

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RESULT 15
US-09-430-323-24
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09430323 Patent No. 6309867 GENERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                         ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PETENTIA Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R.
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                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                  APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP
CATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
Chapman, Karen B.
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Pred. No. 0.0075;
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                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                            Matches
                                                                                                                Query Match
                                                                          / Match 59.1%;
Local Similarity 91.7%;
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                              7 ICHQIEYYFGDF 18
ICHQ-EYYFGDF 11
                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                            0; Mismatches
                                                                                            Score 58.5; DB 4; Length 37; Pred. No. 0.0075;
                                                                            0; Indels
                                                                          1.
                                                                            Gaps
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Search completed: September 10, 2004, 18:05:09 Job time : 15.8883 secs

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APPLICANT: Molli,
APPLICANT: Harley, Calvin
APPLICANT: Harley, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-721-456-215
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 215: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                 APPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997
APPLICATION NUMBER:
                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-APR-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cecn,
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90.9%;
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US 08/846,017
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Sequence 24, Ap
Patent No. 6261
                                              FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-02
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcad
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
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CLASSIFICATION:
                                                                                                                                                                            APPLICATION NUMBER:
                APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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T: Morin, Gregg B.
T: Harley, Calvin
T: Andrews, William H.
INVENTION: No. 6261836el Telomerase
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                                                                                                                                                                                                                                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lingner, Joachim
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91.7%;
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Pred. No. 0.0075;
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US-09-402-181B-215
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SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 10; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 215, Application US/09402181B
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-196
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNES, CONTROL OF THE PARK TO NAME: Apple, Kanucry Name: Apple, Recurstration NUMBER: 36,429
REGISTRATION NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHAX: (415) 576-0300
TELEPHAX: 415) 576-0300
                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ichoiexxecb 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICEQIEYYFGD 11
                                                                 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                         APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                        APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Harley, Calvin B.
Andrews, William H.
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Nakamura, Toru
Chapman, Karen B.
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Pred. No. 0.0064;
0; Mismatches
US 08/854,050
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US-09-721-456-215
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
CORRESPONDENCE Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICEQIEYYFGD 11
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakāmura, Toru
Chapman, Karen B.
Morin, Gregg B.
Marin, Gregg B.
Harley, Calvin B.
Andrews, William H.
OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                      APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
  APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 38 amino acids
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Pred. No. 0.0064;
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DB 4;

1; Indels Length 38;

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Gaps

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RESULT 11

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

09-MAY-1997

APPLICATION NUMBER:

14-AUG-1997

US 08/911,312

FILING DATE:

06-MAY-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NOWMENT OF THE NAME OF THE NAME OF THE NAME OF THE NAME APPLE, RANDOLPH TED REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-002610US
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                   APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                               ZIP: 94111
                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                             FILING DATE: 09
CLASSIFICATION:
                                                                                                                                                                                                  COUNTRY:
                                                                APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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10; Conserv
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Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
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                                                                                                                                                                                                    United States of America
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                                  .umbER: US/08/854,050
09-MAY-1997
N: E27
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                                                                                                                                                                                                                                                                                                                                                                                       Karen B.
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US 08/851,843
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Pred. No. 0.
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Best Local S
Matches 10
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GENERAL INFORMATION:
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TELEPAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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APPLICATION NUMBER: US 08/844,419
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PRIOR APPLICATION DATA:
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                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: CURKNOWN>

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H. TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cech, Thomas R.
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STATE: California
APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
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Nakamura, Toru
Chapman, Karen B.
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FILING DATE: 14-AUG-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS: LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                             PRIOR APPLICATION DATA:
                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Andrews
                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 25-APR-1997
                                                                                                                                   FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                             STREET:
                APPLICATION NUMBER: 18-AP
                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/US97/17618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08851843A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                        E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                                                                                                                                                                                                                                                                                              Andrews, William H. // // No. 6093809el Telomerase
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lingner, Joachim
                UMBER: US 08/844,419
18-APR-1997
                                                                                                                                                   06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas R.
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91.7%;
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                                                                                                 US 08/846,017
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Pred. No.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
               APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997 PRIOR APPLICATION DATA:
                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
APPLICATION NUMBER: US 08/844,449
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
                                                                 FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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STATE: Cal
                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
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STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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Harley, Calvin B.
Andrews, William H.
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                                                                                                         US 08/846,017
US 08/854,050
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Pred. No. 0.0064;
0; Mismatches
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US-09-402-181B-214
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Best Local S
Matches 11
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6610839
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS:
linear
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                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                       APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
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                                                                                                                               APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                    APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                             APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                      APPLICATION NUMBER:
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Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
Andrews, William H.
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Nakamura, 101-
Man, Karen B.
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91.7%;
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ER: 015389-002610US
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Pred. No. 0.
                                      US 08/912,951
US 08/915,503
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214
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US-09-721-456-214
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Patent No. 6617110
GENERAL INFORMATION:
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Best Local Similarity
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PO
FILING DATE: 01-CGT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFEICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
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Lingner, Joachim
Nakamura, Toru
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91.7%;
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        US 08/911,312
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NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
Score 68; DB 4;
Pred. No. 0.00022;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                 PCT/US97/17885
                                Length 38;
   Indels
   0,
   Gaps
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Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit

APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997 APPLICATION NUMBER: US 08/854,050

PRIOR FILING DATE:

1997-10-06

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                          TELEFAX: (404)-873-87
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PELICATION DATA:
                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (404)-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                           NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08, FILING DATE: June 7, 1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: April
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                         LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 1994-10-11
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2800 One Atlantic Center, 1250 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                           (404) -873-8795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
single
linear
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April 13, 1992
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Pred. No. 8.5e-10;
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US-08-974-549A-214
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                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/724,643
FILLING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILLING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILLING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILLING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF PARTY OF TWO Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
FEATURE:
                                   FILING DATE: 14-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER:: US/08/974,549A
                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TILE OF INVENTION:
                                                                                                                                                             APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                      APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                        APPLICATION NUMBER: FILING DATE: 14-AUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-NOV-1997
                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 73.7%;
Local Similarity 100.0%;
es 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214, Application US/08974549A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harley, Calvin B.
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8..15
                                                                                                        TUMBER: US 08/912,951
14-AUG-1997
JMBER: WO PCT/US97/17618
01-OCT-1997
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Human Telomerase Catalytic Subunit
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; Pred. No.
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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   222321177
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length: 2000000000
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99
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AALEAKICHQIEYYFGDF 18
             Copyright
   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51625971 residues
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                    US-09-316-630-3
US-09-316-630-4
US-08-475-955-20
US-08-475-955-20
US-08-974-549A-214
US-09-402-181B-214
US-09-402-181B-215
US-08-851-843A-25
US-08-854-050-25
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US-09-402-181B-215
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US-08-851-843A-24
US-08-851-843A-26
US-08-854-050-26
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US-08-974-549A-216
US-08-974-549A-216
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US-08-205-719-4
US-08-431-517F-5
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             US-09-489-039A-9103
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Sequence 3, Appli
Sequence 4, Appli
Sequence 214, App
Sequence 214, App
Sequence 214, App
Sequence 215, App
Sequence 25, Appl
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Sequence 25, Appl
Sequence 215, App
Sequence 215, App
Sequence 214, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 216, Appl
Sequence 310, Appl
Sequence 4, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
             Patent No.
Sequence
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41 41.4 1220 2 US-08-680-326-38 40 40.4 431 US-08-311-023-2 40 40.4 593 4 US-09-252-991A-23340 40 40.4 593 4 US-09-800-729-106 40 40.4 686 4 US-09-800-729-199 39 39.4 692 4 US-09-675-594-733 39 39.4 754 2 US-08-941-262-3 39 39.4 811 1 US-08-941-262-3 39 39.4 812 1 US-08-248-629A-1 39 39.4 812 1 US-08-248-629A-1 39 39.4 812 1 US-08-248-629A-1 39 39.4 812 1 US-08-278-785-1 39 39.4 812 1 US-08-326-785-1 39 39.4 812 2 US-08-615-598B-1 39 39.4 812 2 US-08-615-598B-1 39 39.4 812 2 US-08-625-598B-1
1220 431 868 921 431 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
0 1 4 4 4 4 0 0 4 1 1 1 1 0 0 0 0 0 0 0
US-08-680-326-38 US-08-311-023-2 US-09-801-729-106 US-09-800-729-106 US-09-800-729-7385 US-09-976-594-733 US-09-976-594-733 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-41-932-1 US-08-451-932-1 US-08-451-932-1 US-08-451-932-1 US-08-451-938-1 US-08-615-785-1 US-08-605-598B-1 2 US-08-605-598B-1 2 US-08-625-743-1
US-08-680-326-38 US-08-311-023-2 US-09-252-991A-23340 US-09-800-729-106 US-09-800-729-199 US-09-800-729-1385 US-09-976-594-733 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-3 US-08-941-262-1 US-08-199-637A-93 US-08-199-637A-93 US-08-248-629A-1 US-08-248-629A-1 US-08-451-932-1 US-08-451-932-1 US-08-451-938-1 US-08-612-788-1 US-08-612-788-1 US-08-612-788-1 US-08-612-788-1

RESULT 1

ALIGNMENTS

US-09-316-630-3

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APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IR
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CR
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1994-10-06
PRIOR FILING DATE: 1994-10-11
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                                                                                                                                                                                                                                                                                       US-09-316-630-4
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/90/316,630
CURRENT APPLICATION NUMBER: US/90/316,630
PRIOR APPLICATION NUMBER: 08/817,953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09316630
Patent No. 6291637
                                                                                                                                                                                                                                  Sequence 4, Application US/09316630 Patent No. 6291637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 99; DB 3; ilarity 100.0%; Pred. No. 8.5e-10; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRES-MEDIATED TRANSLATION BY A CRITICAL RNA-PROTEIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC associated with breast and ovarian cancer. Included in the invention are CC sequences AAP22032 - AAP22040 and AAB59129 which are used in the CC isolation and characterisation of the DNA and protein sequences of the CC invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antivilcer; vulnerary; anticonvulsant; antidiabetic; antiinflammatory; antivilcer; vulnerary; anticonvulsant; antibacterial; antiinflammatory; antivilcer; vulnerary; anticonvulsant; antibacterial; cc antifungal; antiparasitic and cardiant activity. The polynucleotide and C protein sequences are used in the diagnosis of cancer, particularly cc breast and ovarian cancer. The nucleic acid sequences, proteins, agonists cand agonists may also be used in the diagnosis, prevention and treatment confimmune disorders e.g. Addison's disease, autoimmune consecutar disorders such as myocardial ischeems mellitus, Crohr's cardiovascular disorders such as myocardial ischaemias; wound healing; conversioned and disorders such as myocardial ischaemias; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
               Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
                                                                                                            Human ovarian antigen HVVAF56,
                                                                                                                                                                                                                          ABP41511 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAF21614 - AAF22031 represent DNA sequences encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 1149-11150; 1299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and diagnosis of cancer, immune disorders, neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US005881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                  22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins AAB58711 - AAB59128. The DNA and protein sequences are
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DB; AAF21890.
                                                                                                                                                                                                                                                                                                                   63
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                                                                                                                                                                                                                          protein; 460
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
immune disorder; blood disorder;
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                                                                                                            SEQ ID NO:2643.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epilepsy;
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Search completed: September 10, Job time: 56.4128 secs

2004, 17:51:48

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AALEAKICHQIEYYFGDF

80

Matches Query Match

18; Similarity

Conservative

<u>,</u>

100.0%;

Score 99; DB 5; 1 Pred. No. 3.2e-07; Mismatches

Length 460; Indels

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AALEAKICHQIEYYFGDF

Local

Sequence

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CC recombinant vectors and host cells comprising human ovarian antigen of ovarian antigen polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, conference of ovarian antigens of preventing various ovary and/or breast related disorders. Such conditions include ovarian concer and breast cancer, and conference of disorders. Such conditions include ovarian cancer and breast cancer, and concern disorders, infections (e.g., infertility, disorders of pregnancy, anovulation, conjugated by syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), inflammatory conditions (e.g., mastitis, oophoritis and communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), conspiratory disorders, neurological disorders, gastrointestinal disorders, candurates ovarian antigen polypeptides and conjugated disorders. Ovarian antigen polypeptides and conjugated by used in screening for compounds which conjugated by used in screening for compounds which conjugated by used as food additives or to prepare antibodies and the sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed cate for wino infrant/published not sequence format directly from WIPO at the properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 2175 novel numan ovarian analysis (REP43228) and to cDNAs encoding them (ABQ5431-ABQ56305), and also ancompasses polypeptides 90% identical and polynocleotides 95% identical encompasses polypeptides 90% identical monoton additionally relates to to the sequences of the invention. The invention additionally relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cyrostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 2643; 2922pp; English
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                                         at ftp.wipo.int/pub/published_pct_sequences
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460 AA;
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RESULT 13
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Ct that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates CC the expression of a polymucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a CC compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a CC polymucleotides, a method for producing a pharmaceutical composition, a CC polymucleotides, a method for producing a pharmaceutical composition, a cctivity in an animal of one or more of the polypeptides given in the CC specification, a method for identifying a compound useful in treating CC pain and a pharmaceutical composition comprising the one or more CC polypeptides or their antibodies. The polymucleotide or the compound that CC modulates its activity is useful for preparing a medicament for treating CC pain (e.g. spinal segmental nerve injury (CNINg), chronic constriction CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene CC the specification) which is differentially expressed during pain. Note: CC the specification, but was obtained in electronic form directly from WIPO at CC francia introducional contraction of the printed CC specification, but was obtained in electronic form directly from WIPO at CC francia contraction will call and contraction will call and contraction will call and contraction of the printed contraction will call and call call and cal
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Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising preparing a medicament for
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB )
                                           Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                                                                                                       ABG08417 standard;
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Homo sapiens
                                                                                                                         Novel human
                                                                                                                                                                         13-FEB-2002
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BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 AA;
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                                                                                                                       diagnostic protein #8408
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                                                                                                                                                                                                                                                                       protein;
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100.0%; Pred. No. 2.8e-07;
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RESULT 14
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Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hew isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asset the contract of the 
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB58987 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AALEAKICHQIEYYFGDF 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                    ovarian cancer associated antigen protein sequence SEQ ID 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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RESULT 11
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  14-AUG-2001; 2001US-0312147P
                                               14-AUG-2002; 2002WO-US025765
                                                                                                                                                      WO2003016475-A2
                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                     Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                             Rat Protein P38656, SEQ ID NO 9935.
                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE63989 standard; protein; 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 AA;
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a composition comprising two
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Pred. No. 2.8e-07;
Pred. No. 2.8e-07;
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ADE63993

ADE63993 standard; protein; 415

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RESULT 12

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29-JAN-2004 ADE63993;

(first entry)

Rat Protein P38656, SEQ ID NO 9939.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

27-FEB-2003

WO2003016475-A2 Rattus norvegicus

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                                                                                                                                                               that is differentially expressed in neuronal tissue of a first animal consumers of the pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the compound for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more composition to the polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating composition composition composition (e.g. spinal segmental nerve injury (Chung), chronic constriction composition (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the property of the specification of the patent of the printed specification is proventially expressed during pain.
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Matches
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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26-NOV-2001; 2001US-0333347P.
                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which is differentially regulated in an animal subjected to pain and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                 Local
1 AALEAKICHQIEYYFGDF 18
                                                            l Similarity
18; Conserv
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BAYER AG.
                                                                                                                                                               415
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                                                            100.0%; Score 99; DB 7; llarity 100.0%; Pred. No. 2.8e-07; Conservative 0; Mismatches 0;
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                                                                                                            DB 7;
                                                                                                            Length 415;
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                                                               Gaps
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Claim 1; Page; 1017pp; English

invention discloses a composition comprising two or more isolated

iragment,

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

GENBANK; P05455

Claim 1; Page; 1017pp; English.

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or human polynucleotides or a polynucleotide which represents a fragmer derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a
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cc kit to perform the method, an array, a method for identifying an agent ct that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal csubjected to pain, a method for identifying an agent csubjected to pain, a method for identifying a compound which regulates ct the expressed in an animal subjected to pain, a method for identifying a compound which regulates compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound that regulates the cc method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating compound and a pharmaceutical composition comprising the one or more compound that regulates its activity is useful for preparing a medicament for treating compain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (CNINg), chronic constriction confictation) which is differentially expressed during pain. Note: The specification, but was obtained in electronic form directly from WIPO at the printed but was obtained in electronic form directly from WIPO at the printed of the prin ftp.wipo.int/pub/published_pct_sequences.

Sequence 408 AA;

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RESULT 9
ADE63995
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Best Local S
Matches 18
                                                                                                                                          Human Protein P05455, SEQ ID NO 9941.
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                                                                                                                                                                             ADE63995 standard; protein; 408 AA.
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                                                                                                                                                                                                                       1 AALEAKICHQIEYYFGDF
                                                                                                                                                                                                                                            Similarity
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Human; spinal

nerve

injury; SNI; Chung.

pain; neuronal tissue; gene therapy; segmental nerve injury; chronic cons

constriction injury; CCI;

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

GEN HOSPITAL BAYER AG.

CORP

14-AUG-2002; 2002WO-US025765

27-FEB-2003 WO2003016475-A2 Homo sapiens

WPI; 2003-268312/26

Woolf C,

D'urso D,

Befort

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Costigan M;

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Colaimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence comprising the vector, a method for identifying a nucleotide sequence contains a differentially regulated in an animal subjected to pain and a contain that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the continucleotide, a method for producing a pharmaceutical composition, a compound for identifying a compound or small molecule that regulates the continuity in an animal of one or more of the polynucleotide or their animal of one or more of the colypeptides or their antibodies. The polynucleotide given in the colypeptides or their antibodies. The polynucleotide or the compound that new continuity (cnums), chronic constriction constriction (e.g. spinal segmental nerve injury (cnums) a medicament for treating continuity (constriction) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed at for its patent did not form part of the printed at for its patent did not form directly from WIPO at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or the part of the printed at the confidential or 
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Sequence 408
                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
              AA,
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Best Loc Matches Query Match Local 11 1 AALEAKICHQIEYYFGDF 18 18; Similarity AALEAKICHQIEYYFGDF 100.0%; Score 99; DB 7; llarity 100.0%; Pred. No. 2.8e-07; Conservative 0; Mismatches 0; 28 Length 408; Indels 0 Gaps

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RESULT 10
ADE62859
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01-NOV-2001;
26-NOV-2001;
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spinal
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(GEHO ) GEN HOSPITAL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
                                                                                            ; 2001US-0312147P.
; 2001US-0346382P.
; 2001US-0333347P.
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proteins that are implicated in a specific

present invention relates to methods for identifying genes and eins that are implicated in a specific disease or physiological

Claim 35; Page 425; 538pp; English

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RESULT 7
ADE63991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  condition. The method comprises comparing the transcriptome proteome of a condition. The method comprises comparing the transcriptome of a condition with that of a second specialised cell type implicated in a disease or condition with that of a cell type, under two experimental conditions, and conditions, and conditions are useful for the two specialised cell types under experimental conditions. ABV7873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesss, angiogeness, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
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Best Local
The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
                                                                   Claim 1;
                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                       WPI; 2003-268312/26
GENBANK; P05455.
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(FARB )
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003016475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Protein P05455, SEQ ID NO 9937.
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                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002; 2002WO-US025765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                                                                                          BAYER
                                                                   Page; 1017pp;
                                                                                                                                                                                                     D'urso D,
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                                                                                                                                                                                                       Befort K,
                                                                   English
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                fragment,
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RESULT 8
ADD46272
ID ADD4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC that increases or decreases the expression of the polymucleotide sequence considered to pain, a method for identifying a compound which regulates compound that regulates compound that regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound or small molecule that regulates the activity of one or more of the cartivity in an animal of one or more of the polymucleotides, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polympeptides given in the capture of the polympeptides of the capture of the polympeptides of the compound that regulates the compound or more of the polympeptides or their antibodies. The polymucleotide or the compound that condulates its activity is useful for preparing a medicament for treating compain (e.g. spinal segmental nerve injury (Chung), chronic constriction compain (e.g. gene context). The sequence presented is a human protein (shown in Table 2 of the specification, which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed conscription in the polymperise description which is different of the printed conscription that the polymperise description which is different to the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                       (GEHO )
(FARB )
                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 408 AA;
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                                                                                        WPI; 2003-268312/26.
GENBANK; P05455.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Protein P05455, SEQ ID NO 11947
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                                                                                                                                                             Woolf C,
                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2002;
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nerve injury; SN
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                                                                                                                                                           D'urso D,
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larity 100.0%;
Conservative 0
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2001US-0346382P.
2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                            2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                injury; SNI; Chung.
                                                                                                                                                                                                                                  CORP
                                                                                                                                                             Befort
                                                                                                                                                             <u>,</u>×
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Pred. No. 2.8e-07;
                                                                                                                                                             Costigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 408;
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gene therapy; chromosome mapping

Mon

WPI; 2000-500381/45 Dumas Milne Edwards J,

Duclert

P

Giordano

AAC01357

26-FEB-1999;

99US-0122487P

(GEST) GENSET

21-FEB-2000; 2000EP-00200610

06-SEP-2000 EP1033401-A2 Homo sapiens

Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.

diagnostic, forensic, gene therapy and chromosome mapping procedures.

New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond

tag (5' EST) for to 5'EST8 and fo

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RESULT 5
AAW03716
ID AAW0
XX AAW0
AC AAW0
DT 25-M
DT 12-M
XX Huma
XX Huma
XX Syst
KW Syst
XX Syst
CX WS Homc
XX US5:
XX O30-:
XX 31-1
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                                                                         Homo sapiens
                                                                                           Autoimmune
systemic lu
                                                                                                                      Human autoantigen La(SS-B).
                                                                                                                                         25-MAR-2003
12-MAR-1997
 31-DEC-1984;
                   27-MAY-1987;
                                                                                                                                                                    AAW03716
                                     30-JUL-1996
                                                        US5541291-A
                                                                                                                                                                                      AAW03716 standard;
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                                                                                                                                                                                                                                             1 AALEAKICHQIEYYFGDF 18
                                                                                           Lupus
                                                                                                                                                                                                                                     AALEAKICHQIEYYFGDF
                                                                                                   disease;
                                                                                                                                        (revised)
(first entry)
                                                                                            erythematosus;
  84US-00687908
                   87US-00054871
                                                                                                                                                                                      protein;
                                                                                            La autoantigen; Sjo
hematosus; diagnosis
                                                                                                                                                                                                                                     28
                                                                                                                                                                                       ₽
                                                                                                    Sjogren's syndrome;
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S

Query Match Best Local S Matches 18

Similarity

100.0%;

Score 99; Pred. No.

5.8e-08; DB 3;

Length 92;

18;

Conservative

0

Mismatches

Indels

0

Sequence 92

AA;

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5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polya+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and even in those cases where therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence is a polypeptide encoded by one of a large number of ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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ABP65252
ID ABP6
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Best Local S
Matches 18
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                            Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two celtypes under different conditions and identifying a differentially
                                                                                                                                                                                                                                08-DEC-2000; 2000GB-00030076
08-FEB-2001; 2001GB-00003156
25-OCT-2001; 2001GB-00025666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma overlap syndrome - useful for diagnosis and treatment of autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-362015/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;
hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; antiinflammatory; vulnerary; gynecological; ophthalmologica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypoxia-regulated protein #126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP65252;
                                                                                                      WPI; 2002-627238/67.
                                                                                                                                        Rayner
                                                                                                                                                          White J,
                                                                                                                                                                                                                                                                                                                                          13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                             WO200246465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preeclapmsia;
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              regulated
                                                                                                                                                                                                                                                                                                        10-DEC-2001; 2001WO-GB005458
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library.
                                                                                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation;
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             gene.
                                                                                                                                                          Mundy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                          CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 408
                                                                                                                                                          Ward NR,
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Pred. No. 2.8e-07;
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                                                                                                                                                          Kingsman
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                                                                                                                                                              Harris
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rhinovirus,

duck

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                                                                                                                                                                                                                      The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhabdovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovicoxsackie virus, encephalomyocarditis virus, foot-and-mouth disease virus, echo virus, hepatitis C virus, infectious bronchitis virus, di and human hepatitis B virus, and vesicular stomatitis virus. The pept also inhibits replication of the above viruses. The LAP peptide selectively inhibits viral protein translation, and is therefore not toxic to the host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 15; 19pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-2001; 2001US-00836073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

Human secreted

protein,

SEQ ID NO: 5432

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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	₅	4	ω	N	1	Result No.
84	87	87	87	88.5	90	91	91			99		99	99	99	99	99	99	99	99	99	99	99	99	99	Score
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Abg72107 Viral rep	Viral	Viral	Viral	Viral	Viral	Viral		Viral	Abg72113 Viral rep		Aab58987 Breast an	Abg08417 Novel hum		Ade63989 Rat Prote	Ade62859 Human Pro	Ade63995 Human Pro	Add46272 Human Pro		Abp65252 Hypoxia-r	Aaw03716 Human aut	Human	Viral		-	Description

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Abm48977	Aau52458	Ada55336	Abb89645	Abg27058	Abg72117	Abu43510	Aag47712	Aag47713	Aag47714	Abm72091	Abj19009	Abp70526	Abb65316	Abg72119	Abg72106	Aar43394	Abg72105	Abg72115	DOTE STORY
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ALIGNMENTS

RESULT 1

La autoantigen; LAP; internal ribosome entry site; IRBS; translation; viral replication; IRNA; antiviral agent; picornavirus; flavivirus; coronavirus; hepatitis virus; rhabdovirus; adenovirus; coxsackte virus; parainfiluenza virus; poliovirus; rhinovirus; encephalomyccarditis virus; foot-and-mouth disease virus; echo virus; infectious bronchitis virus; Human la autoantigen peptide (LAP). 14-MAR-2000 AAY52200; 02-DEC-1999. WO9961613-A2. vesicular stomatitis virus. AAY52200 standard; Homo sapiens. (first entry) peptide; 18 A

21-MAY-1999; 99WO-US011281

22-MAY-1998; 98US-0086527P

(REGC) UNIV CALIFORNIA.

Das S, Dasgupta A;

WPI; 2000-062712/05.

New yeast inhibitory peptide useful for inhibiting viral protein translation and replication.

Claim 5; Page 57; 81pp; English.

This sequence is the La autoantigen binding domain (LAP). LAP is a cellular protein which binds to an internal ribosome entry site (IRES). The peptide is used to inhibit mRNA translation, viral protein translation or viral replication. Viral mRNA translation is initiated at the IRES and the LAP peptide prevents translation initiation factors from binding at the site. The peptide can be used alone or in combination with an inhibitor RNA (IRNA see AAZ45200). The LAP peptide is useful as an antiviral agent, which works through the inhibition of mRNA translation, especially viral mRNA. Examples of viruses which can be inhibited are picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,

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Search completed: September 10, 2004, 18:11:55 Job time : 40.424 secs

Page 5

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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
CENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-11
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US-09-836-073-10
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; ORGANISM: Homo Sapiens
US-09-836-073-10
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GENERAL INFORMATION: Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Narayan
APPLICANT: Baidya, Narayan
TITLE GENERALCE: 200002054822
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                        Sequence 16, Application US/09836073 Patent No. US20020173475A1 GENERAL-INFORMATION:
                                               NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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Best Local :
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Best Local Similarity
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                                                                                                     APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                   LENGTH:
TYPE: PR
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ORGANISM: Rat
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Local Similarity B8.9%;
les 16; Conservation
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88.9%;
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Pred. No.
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Pred. No. 1.9e-06;
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2.7e-06;
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APPLICANT: Dasgupta, Asim
APPLICANT: Dasy S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                               ; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-3
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US-09-836-073-3
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                                                  Query Match
Best Local Similarity 77.8
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Best Local Similarity
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE BOT INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
CURRENT FILING DATE: 2002-10-24
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AALQAKICHQIQYYFGQF 18
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83.3%;
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                                                              Score 79; DB y; LC
Pred. No. 8.2e-06;
No. 8.2e-06;
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Pred. No. 8.2e-06;
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Sequence 8, Application US/09836073

Patent No. US20020173475A1

GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822

CURRENT APPLICATION NUMBER: US/09/836,073

CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
INMBER OF SEQ ID NOS: 4360
SOCTWARE: PATENTIN Ver. 3.1
SEQ ID NO 2643
LENGTH: 460
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US-10-264-049-2643
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US-09-836-073-8
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Best Local Similarity
Matches 17; Conserv
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA133P1
                                                                                                                                      TYPE: PRT ORGANISM: Homo Sapiens
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                                                                                                                                                                           LENGTH: 18
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94.4%;
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94.4%;
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Pred. No. 2.7e-06;
                                                             Score 89; DB 9;
Pred. No. 2e-07;
0; Mismatches
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                                                                                             Length 18;
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APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REF
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
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US-09-836-073-13
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; Sequence 11, Application US/09, Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim APPLICANT: Das dya, Narayan TITLE OF INVENTION: METHODS TV
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US-09-836-073-11
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US-09-836-073-9
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LENGTH: 17
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Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
TITLE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
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Best Local Similarity
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ORGANISM: Mouse
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                                                                                                              Application US/09836073
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                                                                                                                                                                                                                                                                                                   87.6%;
94.1%;
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   TO INHIBIT VIRAL REPLICATION
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Pred. No.
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Pred. No. 8.8e-07;
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US-09-836-073-14
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1
                                                                                                                                                                                                                                                                             US-10-170-385-477
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
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SEQ ID NO 14
LENGTH: 18
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity
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                                                                                                                                                                                                                                         Sequence 477, Application US/10170385 Publication No. US20030203372A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bovine
-09-836-073-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REPERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR EPILING DATE: 1999-05-21
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CURRENT FILLNG DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OP INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
                                                                                 APPLICANT:
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                                                                                                                                                                                                        APPLICANT: Ward, Neil Raymond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/10/170,385
                                                                                                     APPLICANT:
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                                                                             Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                  Harris, Robert Alan
White, Jonathan
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Pred. No.
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Sequence 695, Application US/09925298

Publication No. US20020039764A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA103

CURRENT APPLICATION NUMBER: US/09/925,298

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: PCT/US00/05881

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 846

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 695

LENGTH: 460
                                                                                                                                                                                                                                                        RESULT 6
US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: ROSen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins
; FILE REFERENCE: PA103plC1
; FILE REFERENCE: PA103plC1
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US-09-925-298-695
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                                                              CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
LENGTH: 460
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Best Local Similarity 94.4%;
Matches 17; Conservative
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PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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les 17; Conserva
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Pred. No. 2.7e-06;
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2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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/ cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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12 US-10-102-806-695
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15 US-10-264-049-2643
US-09-836-073-13
US-09-836-073-13
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Sequence 12, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 477, App
Sequence 695, App
Sequence 695, App
Sequence 2643, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
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US-10-094-749-2904	US-10-437-963-201436	-963-11176	9	US-10-210-130-66	- 1	US-10-437-963-200899	US-10-437-963-200901	US-10-282-122A-49328	US-09-836-073-19	4	10-054-295-	758-2	09-438-486-		US-09-843-676-24	4-61	N	US-10-053-758-25	US-10-325-810-215	US-09-438-486-25	US-09-766-253-25	-676-2	US-10-325-810-214	10-376-121A-2	36-073-5	9-836-073-	9-836-073-6	9-836-073-	US-09-836-073-4
Sequence 2904, Ap	e 201436	Sequence 111769,	e 6, 4	e 66, AL	1854	e 200899	æ	e 4.	19,	e 24	e 24,	24,	24	24,	24,	ര	e 25	e 25	e 215,	e 25, 1	25,	25	e 21	2 9	5, A	e 15,	0 6	Sequence 7, Appli	e 4

ALIGNMENTS

RESULT 1 US-09-836-073-12

Sequence 12, Application US/09836073 Patent No. US20020173475A1

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Dasdy, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR REPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-12
US-09-836-073-1
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dassupta, Asim
; APPLICANT: Das, S.
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Best Local S
Matches 18
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                                                                                                                                                               Similarity
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100.0%; Pred. No.
tive 0; Mismatch
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-CLASSIFICATION: 536

18-APR-1997

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RESULT 15
US-09-430-323-24
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: armino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.:
Best Local Similarity 83.:
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rele
MOLECULE TYPE: pepti
                                                                                                                                                                                                                                                                                        ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PStentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
                APPLICATION NUMBER: US 08/854,050
FILLING DATE: 09-MAX-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICHOIEYOFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America
APPLICATION NUMBER: US 08/724,643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
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LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24
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                                                                                                                                                                                                                                                            FILING DATE: 01-OCT-1996

NAME: APPIe, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
1 ICHQ-EYYFGDF 11
                           7 ICHQIEYQFGDF 18
                                                                   Conservative
                                                                                    52.1%;
83.3%;
                                                                                    Score 50.5; DB 4; Pred. No. 0.065;
                                                                     Mismatches
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                                                                     Indels
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Search completed: September 10, 2004, 18:05:09 Job time: 16.8883 secs

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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6093809
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLAN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                              APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                              FILING DATE:
CLASSIFICATION
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ICHQIEYQFGD 17
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                                                                                                                                                                                                                            San Francisco
: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICEQIEYYFGD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: US 08/911,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08851843A
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                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                      Lingner, Joachim
Nakamura, Toru
                                                                                                                                                                                                            United States of America
                                                                                                                                                                                                                                                                                                                                                                                                       Chapman,
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                                                                                                                                                                                                                                                                                                                                                                                                         Karen B.
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                                                                 US/08/851,843A
US 08/846,017
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Pred. No. 0.055;
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                                                                                                       Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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US-08-854-050-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
US 08/846,017
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
APPLICANT: NICENTICUS: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcad
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 09-MA
                                                                                                                                                                                                                                                                                                                         COUNTRY:
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              APPLICATION NUMBER: FILING DATE: 25-AP
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CLASSIFICATION:
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83.3%;
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RESULT 11
US-09-402-181B-215
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 9; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                            APPLICATION NUMBER: US/09/402,181B FILING DATE: 29-Sep-1997 CLASSIFICATION - «Unknown» APPLICATION DATA:
                                                             APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ICEQIEYYFGD 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
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                      APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF SEQUENCES: 633
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Chapman, Karen B.
Morin, Gregg B.
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81.8%;
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Pred. No. 0.055;
US 08/854,050
                                                                                                                                                                                                                                                                                                       Version #1.30
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US-09-721-456-215
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Matches
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GENERAL INFORMATION:
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REGISTRATION NUMBER: 42,271
REGISTRATION NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
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                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
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STRANDEDNESS: <Unknown>
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                      APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                          CLASSIFICATION: <Unknown>
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US 08/846,017
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Pred. No. 0.055;
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FILING DATE:

09-MAY-1997

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MOLECULE TYPE:

US-08-974-549A-215
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                APPLICANT: Harley, Carrell H. APPLICANT: Andrews, William H. APPLICANT: Andrews, William H. APPLICANT: No. 6261836el Telomerase OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES: Townsend and Townsend and Crew LLP
ADDRESSES: Two Embarcadero Center, 8th Floor
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
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            APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 CLASSIFICATION: 536 AIOR APPLICATION DATA:
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                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
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APPLICATION NUMBER:
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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                                                                                                                                                Floppy disk
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US 08/851,843
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Pred. No. 0.
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Matches
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Patent No. 6309867
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTON NUMBER: 36,429
REFERENCE DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 06-MAY-1997
CLASIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDENMESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                  ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/09/430,323
FILLING DATE: 29-OCT-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero
APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                              COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09430323
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Nakamura, Karen B.
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Harley, Calvin
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Nakamura, Toru
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81.8%; Pred. No. 0.
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RESULT 7
US-08-851-843A-25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 18-APR-1:
CLASSIFICATION:
                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMERR: US/08/851,843A FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                         ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                               United States of America
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Chapman, Karen B.
Morin, Gregg B.
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            UMBER: US 08/844,419
18-APR-1997
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Pred. No. 0.0015;
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RESULT 8
US-08-974-549A-215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cech,
APPLICANT: Lingne
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                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                 APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                   APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
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                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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Local Similarity 81.8%;
Nes 9; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
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REGISTRATION NUMBER: 36,
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5. 6166178
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Chapman, Karen B.
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                                  06-MAY-1997
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US 08/854,050
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Matches
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,429 REFERENCE/DOCKET NUMBER: 01. TELECOMMUNICATION INFORMATION: TELECHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION UMMER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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STATE: California
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                                                                                                                                                                                                         APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                           APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                                                                   APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                                                                              APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
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Nakamura, Torr
Nakamura, Karen B.
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Pred. No. 0.0015;
US 08/915,503
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US-09-721-456-214
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Best Local Similarity
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APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <UNKnown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Nakamura, Toru
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
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TELEFAX: (415) 5
                                                                                         APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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STATE: California
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                                     APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
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Pred. No. 0.
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7.0015;
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Gaps

APPLICATION NUMBER: FILING DATE:

1994-10-11 1997-10-06

08/321,427

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                                    TELEFAX: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino
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SEQ ID NO 4
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APPLICANT: Harley
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TYPE: PRT
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                                                                                                                                 NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OWRF114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/648,205 FILING DATE: January 31, 1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,
FILING DATE: April 13, 1992
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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               LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 1998-05-22
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2800 One Atlantic
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ss: single
linear
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antic Center, 1250 West Peachtree Street
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Pred. No.
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RESULT 4
US-08-974-549A-214
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                             FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 19-NOV-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                  PRIOR APPLICATION DATA:
                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFILICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
ANIMADER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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LOCATION:
                                                     APPLICATION NUMBER: FILING DATE: 14-AUG
                                                                                                           APPLICATION NUMBER: FILING DATE: 14-AUC
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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Chapman, Karen B.
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Andrews, William H.
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8..15
                                                                                                         UMBER: US 08/912,951
14-AUG-1997
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                                                UMBER: US 08/915,503
14-AUG-1997
JMBER: WO PCT/US97/17618
01-OCT-1997
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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  pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                    length: 0
length: 2000000000
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Match
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97
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Gapop 10.0 ,
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                       Copyright
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  GenCore version (c) 1993 - 2004
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           US-09-316-630-4
US-08-475-955-20
US-08-475-955-20
US-08-475-955-20
US-08-974-549A-214
US-09-402-181B-214
US-09-402-181B-215
US-08-851-843A-25
US-09-430-333-25
US-09-421-456-215
US-09-421-456-215
US-09-430-323-24
US-09-430-323-24
US-08-851-843A-24
US-08-851-95-19-4
US-08-431-517F-6
US-08-431-517F-6
US-08-431-517F-5
5245013-2
US-08-851-843A-26
US-08-851-843A-26
US-08-854-050-26
US-08-854-050-26
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US-08-851-843A-26
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Compugen Ltd.
Sequence 3, Appli
Sequence 4, Appli
Sequence 214, App
Sequence 214, App
Sequence 214, App
Sequence 215, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 27, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 26, Appli
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	39	39	39	39	39	39	39	39	39	40	40	40	40	40	40	40	40	40
	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2	41.2
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ALIGNMENTS	US-08-451-932-1	US-08-248-629A-1	US-09-199-637A-93	US-09-148-545-237	US-09-148-545-179	US-08-937-067-2	US-08-937-067-4	US-09-234-613-15	US-08-933-750C-15	US-08-899-232-2	US-08-532-384-20	US-08-083-590A-20	US-08-185-432-17	US-09-113-825-2	US-08-537-210A-2	US-09-252-991A-25861	US-09-027-166-7	US-09-721-456-216
	sequence I, Appli	٠,	٠,٧		179	2, A	4, 0		Sequence 15, Appr	Sequence 2, Appri	2	2 0	Sequence 17, Appl		,) (

밁 US-09-316-630-3 FILE REFERENCE: 22000-20548.21 CURRENT APPLICATION NUMBER: US/09/316,630 CURRENT FILING DATE: 1999-05-21 PRIOR APPLICATION NUMBER: 08/817,953 PRIOR FILING DATE: 1997-10-06 PRIOR APPLICATION NUMBER: 08/321,427 PRIOR FILING DATE: 1994-10-11 PRIOR APPLICATION NUMBER: 60/086,527 PRIOR FILING DATE: 1998-05-22 NUMBER OF SEQ ID NOS: 4 SOFTWARE: PatentIn Ver. 2.1 US-09-316-630-3 US-09-316-630-4 Sequence 4, Application US/09316630 Patent No. 6291637 GENERAL INFORMATION: Best Loc Matches SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3 LENGTH: 18 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Sequence 3, Application US/09316630 Patent No. 6291637 GENERAL INFORMATION: Query Match APPLICANT: Das, Saumitra APPLICANT: Dasgupta, Asim TITLE OF INVENTION: INTERFERENCE WITH VIRAL TITLE OF INVENTION: SMALL YEAST RNA REVEALS FILE REFERENCE: 22000-20548.21 Local l Similarity 17; Conserv AALEAKICHQIEYQFGDF 18 AALEAKICHQIEYYFGDF Conservative 93.8%; Score 91; DB 3; 94.4%; Pred. No. 3.2e-09; 0 Mismatches Artificial Sequence: IRES-MEDIATED TRANSLATION BY A CRITICAL RNA-PROTEIN INTERACTIONS Length 18; Indels 0 0

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APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
ITTLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548.21
CURRENT FILING DATE: 1999-05-21
CURRENT FILING DATE: 1999-05-21
FRIOR APPLICATION NUMBER: 08/817,953

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                       Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antivicer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; antoimmune themostytic anaemia; autoimmune thyroiditie; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                        08-MAR-2000; 2000WO-US005881.
                                                                                                                                 21-SEP-2000
                                                                                                                                                                  WO200055173-A1
                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               Breast and ovarian cancer associated antigen protein sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB58987 standard; protein; 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                      12-MAR-1999;
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(HUMA-) HUMAN GENOME SCI INC

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are protein sequences are and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agoninvention. The breast and ovarian cancer associated DNA, protein, agoning the protein and characterisation cancer associated DNA, protein, agoning the protein and characterisation cancer associated DNA, protein, agoning the protein and characterisation cancer associated DNA, protein, agoning the protein and characterisation cancer associated DNA, protein agoning the protein and protein accordance and protein acco
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                                                                                                                                               Sequence 460
                                                                                                                                                                                                                                         neurological diseases infectious diseases
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93.8%;
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    Score 91; DB 3;
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Search completed: September 10, Job time: 58.4128 secs

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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                           Rat; pain; neuronal t
chronic constriction
                                                                                                                   14-AUG-2002; 2002WO-US025765
                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                     Rat Protein P38656,
                                                                                                                                                                                                                                       29-JAN-2004
                                                                                                                                                                                                                                                                           ADE63993 standard; protein; 415 AA.
        GENBANK; P38656
                 WPI; 2003-268312/26
                                   Woolf C,
                                                     (GEHO )
(FARB )
                                                                                                                                      27-FEB-2003.
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                                                                                                                                                                                                                                                                                                                                   1 AALEAKICHQIEYQFGDF 18
                                                     GEN HOSPITAL BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                        AALEAKICHQIEYYFGDF
                                  D'urso D,
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                          tissue; gene therapy; spinal segmental nerve injury; n injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                      SEQ ID NO 9939
                                                                                                                                                                                                                                                                                                                                                                    93.8%;
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                                   Befort K,
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Pred. No. 6.9e-07;
0; Mismatches 1;
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Page; 1017pp; English

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a but to parform the method of an area of the respective of the pain and a but to parform the method of an area of the parform the method of the parform the method of the parform the method of the parform the parform the method of the parform the parform the parform the method of the parform the parform the parform the parform the parformance of t

colaimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially the expression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for polynucleotides of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a pharmaceutical composition, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polypuclectide or the compound that polypeptides or their antibodies. The polypuclectide or the compound polypucletides its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence. The invention discloses a composition comprising two ftp.wipo.int/pub/published_pct_sequences specification, but was obtained in electronic represents a or more isolated rat Also fragment,

Sequence 415

AA;

Length 415;

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ftp.wipo.int/pub/published_pct_sequences.

CC kit to perform the method, an array, a method for identifying an agent contract is differentially expressed in neuronal tissue of a first animal contract is differentially expressed in neuronal tissue of a first animal contract the expression of the polynucleotide sequence the expressed in an animal subjected to pain, a method for identifying a compound which regulates contract to pain, a method for identifying a compound which regulates compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a contribution of activity in an animal of one or more of the polypeptides given in the contribution, a method for identifying a compound useful in treating conjunction, a method for identifying a compound useful in treating conjunction, a method for identifying a compound useful in treating conjunction, a method for identifying a compound useful in treating conjunction, a method for identifying a compound that conjunction or more of the polypeptides or their antibodies. The polynucleotide or the compound that conjunction is activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene conjunction) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed conjunction in t

Query Match Best Local S Matches 17 Sequence 415 11 17; 1 AALEAKICHQIEYQFGDF 18 Similarity AALEAKICHQIEYYFGDF Conservative ΑA; 93.8%; 0; 28 Score 91; DB 7; Pred. No. 6.9e-07; Mismatches Length 415; Indels 0 Gaps

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Human; chromosome mapping; gene mapping; gene therapy; forensifood supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                    Novel human diagnostic protein #8408
                                                                                                                                                  13-FEB-2002 (first entry)
                                                                                                                                                                ABG08417;
                                                                                                                                                                             ABG08417 standard;
                                                                                                                                                                             protein; 439
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31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167

(HYSE-) HYSEQ INC.

Tang YT

WPI; 2001-639362/73 Drmanac RT, Liu C, 30-MAR-2001; 2001WO-US008631

11-OCT-2001.

WO200175067-A2 Homo sapiens

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Best Local S
Matches 17
             The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment,
                                                             Claim 1; Page; 1017pp;
                                                                                           New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                              GENBANK;
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(FARB )
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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spinal segmental nerve injury; chronic constriction injury; CCI;
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                                                             English
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Pred. No. 6.
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6.7e-07;
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nucleic

Claim 1; Page; 1017pp; English

New composition comprising two or more isolated polype preparing a medicament for treating pain in an animal

two or more isolated polypeptides,

useful

for

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RESULT 12
ADE63989
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                             27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                         Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat Protein P38656,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADE63989 standard; protein; 415
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                                                                                GENBANK;
                                                                                             WPI; 2003-268312/26.
                                                                                                                              Woolf C,
                                                                                                                                                            (GEHO )
(FARB )
                                                                                                                                                                                                                                                                             14-AUG-2002;
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                                                                                P38656
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Pred. No. 6.7e-07;
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RESULT 9
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ID ADD46272
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ADC ADD4
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Matches 17
                          claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which results the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a
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                                                                                                                                                                                                                                                                                                                         The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
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nerve injury; SN
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Pred. No. 6.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Costigan
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6.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constriction injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating modulates its activity is useful for preparing a medicament for treating modulates its activity (SNI) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
             The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent
                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
'26-NOV-2001; 2001US-0333347P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spinal segmental nerve injury; chronic constriction injury; CCI spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 408 AA;
                                                                                                                                                                                  New composition comprising two or mo preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Protein P05455, SEQ ID NO 9941.
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                                                                                                                                                 Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                      GENBANK; P05455
                                                                                                                                                                                                                                                      WPI; 2003-268312/26
                                                                                                                                                                                                                                                                                   Woolf C, D'urso D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pain; neuronal tissue; gene therapy;
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                                                                                                                                                                                                                                                                                                                      GEN HOSPITAL BAYER AG.
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                                                                                                                                                                                                                                                                                       Befort
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                                                                                                                                                                                  pain in an animal.
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6.7e-07;
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 identifying an polynucleotide
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RESULT 7
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Best Local
                                                                           The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV78116 and ABP65061-ABP65267 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also usef
                                                                                                                                                                                                                                                                                                                                                                              Claim 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two celtypes under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rayner WN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   White J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000; 2000GB-00030076.
08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                regulated gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2001; 2001WO-GB005458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002-627238/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mundy
                                                                                                                                                                                                                                                                                                                                                                         Page 425; 538pp;
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Pred. No.
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6.7e-07
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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, comprising to allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a componing to the polynucleotide sequence kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence composited to pain, a method for identifying an agent compound which regulates the expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the activity of the polynucleotides given in the composition, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more
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spinal
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                                                                                                                                                                                                                                                                                                Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                             New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                       Woolf C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001;
01-NOV-2001;
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(FARB )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                          2003-268312/26.
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segmental nerve injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEN HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408
                                                                                                                                                                                                                                                                                                                                                                             P05455.
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                                                                                                                                                                                                                                                                                                                                                                                                                       D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0312147P.
2001US-0346382P.
2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuronal tissue; gene therapy;
ntal nerve injury; chronic cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                          Befort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO. 9937.
                                                                                                                                                                                                                                                                                                                             two or more isolated polypeptides, useful treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>×
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Pred. No. 6.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constriction
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RESULT 5
AAG01351
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Query Match
Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200283858-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 6; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dasgupta A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2001; 2001US-00836073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2002
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                 06-OCT-2000
                                                                                                                                                                                                                                                                                                   AAG01351 standard; protein; 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
Dumas Milne Edwards J,
                                                  26-FEB-1999;
                                                                           21-FEB-2000; 2000EP-00200610
                                                                                                       06-SEP-2000.
                                                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-058634/05
                                                                                                                                                                                               5' EST;
                                                                                                                                                                                                                                                                                                                                                                                             ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                             AALEAKICHQIEYQFGDF 18
                                                                                                                                                                                                                                                                                                                                                                   AALEAKICHQIEYYFGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                 chromosome mapping.
                                                                                                                                                                                               expressed sequence tag; secreted protein; cDNA isolation;
                                                  99US-0122487P
                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%;
                                                                                                                                                                                                                       SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 91; DB 6;
Pred. No. 2.2e-08;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                        5432.
Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18
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Duclert

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The human lupus antigen (La) is diagnostic for Sjogren's syndrome, well as occurring in systemic lupus erthematosus patients. The La

The La protein

Disclosure;

Co1

15-16;

21pp; English

Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma overlap syndrome - useful for diagnosis and treatment of autoimmune

WPI; 1996-362015/36

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                                ş
                                                                   Matches
                                                                                      Query Match
Best Local
                                                                                                                                                                        The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and even in those cases where therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
N-PSDB; AAC01357.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic, forensic, gene therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs an
                                                                                                                                             Sequence 92 AA;
11
                                1 AALEAKICHQIEYQFGDF 18
                                                                                        Similarity
AALEAKICHQIEYYFGDF
                                                                        Conservative
                                                                                        93.8%;
 28
                                                                      0;
                                                                                          Score
Pred.
                                                                          Mismatches
                                                                                           91;
No.
                                                                   DB 3; Lc...
. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome mapping procedures.
                                                                                                           Length 92;
                                                                          Indels
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                                                                          Gaps
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RESULT 6
AAW03716
ID AAW0
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12-MAR-1997
                                                                                                                                                                                                                                            AAW03716 standard;
                     31-DEC-1984;
                                          27-MAY-1987;
                                                                30-JUL-1996.
                                                                                                                               systemic
                                                                                                                                          Autoimmune
                                                                                                                                                              Human autoantigen La(SS-B)
                                                                                                                                                                                                                      AAW03716;
                                                                                    US5541291-A.
                                                                                                         Homo sapiens
(UYDU-) UNIV
                                                                                                                              lupus
                                                                                                                                          disease;
DUKE
                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                              erythematosus; diagnosis.
                     84US-00687908.
                                          87US-00054871.
                                                                                                                                                                                                                                             protein;
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Query Match Best Local Similarity

100.0%;

Score 97; DB 6; Pred. No. 2.1e-09;

Length 18

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RESULT 2
AAY52200
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                                               Matches
                                                                                            Query Match
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                                                                                                                                                                                                                                                                            This sequence is the La autoantigen binding domain (LAP). LAP is a cellular protein which binds to an internal ribosome entry site (IRES). The peptide is used to inhibit mRNA translation, viral protein translation or viral replication. Viral mRNA translation is initiated at the IRES and the LAP peptide prevents translation initiation factors from binding at the site. The peptide can be used alone or in combination with an inhibitor RNA (IRNA see AAZ45200). The LAP peptide is useful as an antiviral agent, which works through the inhibition of mRNA translation, especially viral mRNA. Examples of viruses which can be inhibited are picornavirus, adenovirus, and parainfluenza virus, poliovirus, rinovirus, coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck and branchitis C virus, infectious bronchitis virus, duck and branchitis C virus, infectious bronchitis virus, duck and branchitis C virus of the contribution of the contributi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Das
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            La autoantigen; LAP; internal ribosome entry site; IRES; translation; viral replication; IRA, antiviral agent; piccornavirus; flavivirus; coronavirus; hepatitis virus; rhabdovirus; adenovirus; coxsackie virus; parainfiluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus; foct and-mouth disease virus; echo virus; infectious bronchitis virus;
                                                                                                                                         Sequence 18
                                                                                                                                                                                                           and human hepatitis B virus, and vesicular stomatitis virus. The pep
also inhibits replication of the above viruses. The LAP peptide
selectively inhibits viral protein translation, and is therefore not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New yeast inhibitory peptide useful for inhibiting viral protein translation and replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-062712/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vesicular stomatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human la autoantigen peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY52200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                             Local Similarity 94.4
les 17; Conservative
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1 AALEAKICHQIEYQFGDF 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 57; 81pp; English.
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                                                                   93.8%;
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Pred.
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                                               Mismatches
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                                                                      91;
No.
                                                                                          DB 3;
                                                                   .2e-08;
                                                                                          Length 18,
                                             Indels
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RESULT 3
ABG72101
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ABG72114
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Matches
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                The present invention relates to peptides and methods of inhibiting the reglication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
                       Viral replication inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compound containing acidic and aromatic amino acids, useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viral replication inhibitor; IRES initiated translation; IAP; internal ribosome entry site initiated translation; La antigen p viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide.
                                                                                                           ABG72114 standard; peptide; 18
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 15; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-058634/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dasgupta A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2001; 2001US-00836073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2002; 2002WO-US011589
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                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replication inhibiting
                                                                                                                                                                                                                                   l Similarity
17; Conser
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                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                     Conservative
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                                                    (first entry)
                                                                                                                                                                                                                                               93.8%;
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                                                                                                                                                                              18
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                  Score 91; DB
Pred. No. 2.26
0; Mismatches
                       peptide, BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide, LAP.
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                                                                                                                                                                                                                               DB 6; h--
. 2.2e-08;
1;
                                                                                                                                                                                                                                                             Length 18;
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Viral replication inhibitor;

IRES initiated translation; LAP;

GenCore version (c) 1993 - 2004

5.1.6 Compugen Ltd.

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Title:
Perfect score:
                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                     Database
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seq
A_Geneseq_29Jan04:*
1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003bs:*
8: geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score. 97 97 91 91 91 91 91 91 91 91	Query Match 93.8 93.8 93.8 93.8 93.8 93.8 93.8 93.8	Length 18 18 18 408 408 408 408	777775236636	ID ABG72112 AAY52200 ABG72101 ABG72114 AAG01351 AAW03716 AAW03716 AAW03716 AAW03716 AAW03716 AAW03991 AAW03991 ADB63991 ADB63995 ADB63995 ADB63995 ADB63989	Description Abg72112 Viral re Aay52200 Human la Abg72101 Viral re Abg72110 Viral re Abg72111 Viral re Abg72111 Human se Aag01351 Human se Aaw03716 Human au Abp65252 Hypoxia Add663991 Human Pr Add663995 Human pr Add663989 Ratt Prot
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16	91		460	σ	ABP41511	Abp41511
17	89		18	თ	ABG72108	Abg72108
18	87		17	თ	ABG72113	Abg72113
19	85		18	σ	ABG72109	Abg7210
20	83		18	σ	ABG72111	Abg72
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22	80.5	83.0	19	σ	ABG72116	Abg72:
23	79	Ļ	18	σ	ABG72102	Abg72102
24	79	Ë	18	Q	ABG72103	Abg72103
25	79		18	σ	ABG72104	Abg72104

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AAB59035	AAM40110	AAM93460	ADA55269	ADA55336	ABB89645	ABG27058	AAU74628	ABB71162	AAU74627	ABP43482	ADE47704	ADA54286	ABU21404	ABG72119	AAR43394	ABG72105	ABG72115	ABG72106	ABG72107
Aab59035	Aam40110	Aam93460	Ada55269	Ada55336	Abb89645	Abg27058	Aau74628	Abb71162	Aau74627	Abp43482	Ade47704	Ada54286	Abu21404	Abg/2119	Aar43394	Abg/2105	Abg/2115	Abg/2106	Abg72107
Breast an	Human pol	Human pol	Human pro	-	Human pol		Oestrogen	Drogophil	Cestrogen	Human sec	Human NOV		Protein e	Viral rep	La/SSD ep	Viral rep			. –

ALIGNMENTS

RESULT 1 ABG72112 ABG72112 ABG72122 AC ABG7 XX ABG72 XX ABG7 XX Vira X Viral replication inhibitor; IRES initiated translation; LAP; internal ribosome entry site initiated translation; La antigen protein; viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide. Viral replication inhibiting peptide, 633. 28-JAN-2003 ABG72112; ABG72112 standard; peptide; 12-APR-2002; 2002WO-US011589. 24-OCT-2002. Unidentified. WO200283858-A2 (first entry) 18 AA.

16-APR-2001; 2001US-00836073.

(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT

Dasgupta A, Das S, Baidya N;

WPI; 2003-058634/05.

New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. as

Claim 10; Page 16; 19pp; English.

The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various biochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 18 AA;

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Search completed: September 10, 2004, 18:11:55
Job time : 40.424 secs

FILE REFERENCE: 220002054822

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RESULT 12
US-09-836-073-12
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; ORGANISM: Homo Sapiens
US-09-836-073-12
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                                 NUMBER OF SEQ ID NOS: 19
SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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APPLICANT: Dasgupta, Asim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09836073 Patent No. US20020173475A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                                                                                                      APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
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TYPE: PRT
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ORGANISM: Homo Sapiens
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Pred. No. 1.9e-05;
0; Mismatches 1
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Pred. No.
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; TYPE: PRT; ORGANISM: Rat
US-09-836-073-16
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US-09-836-073-2
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LENGTH: 18
TYPE: PRT
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Best Local Similarity
Matches 15; Conserv
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SEQ ID NO 16
LENGIH: 19
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                  APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
                                                                 Local Similarity 86. es 13; Conservative
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86.7%;
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                                                                 Score 75; DB 9; 1
Pred. No. 7.9e-05;
1; Mismatches 1.
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Pred. No. 4.8e-05;
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Pred. No. 2.7e-05;
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US-09-925-298-695
                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-102-806-695
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
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                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
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                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                 LENGTH: 460
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                                EAKICHQIEYYFGDF 18
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100.0%; Pred. No
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                                                                                  85.3%; Score 87;
100.0%; Pred. No.
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; Pred. No. 2.4e-05;
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                                                                                  DB 14; 1
. 2.8e-05;
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                                                                                                                                            US-09-836-073-11
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US-09-836-073-9
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SEQ ID NO 9
LENGTH: 18
TYPE: PRT
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LENGTH: 460
                                                                            Sequence 11, Application U Patent No. US20020173475A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%; I
Matches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
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PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
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CURRENT FILING DATE: 2002-10-04
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
                    APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Naraya
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ORGANISM: Homo sapiens
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14; Conservative
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100.0%; Pred. No.
tive 0; Mismatci
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. 9.1e-06;
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2.8e-05;
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Sequence 1, Application US/09836073

Patent No. US20020173475A1

GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PRIOR PRIOR FILING DATE: 1999-05-21

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Matches
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 17
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Best Local Similarity 88.9%;
Matches 16; Conservative
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Da5, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
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TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                          NUMBER OF SEQ ID NOS:
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320020173475A1
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llarity 100.0%; Pred. No. 9.9e-07;
Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: H
US-09-836-073-1
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APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
                           NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 477
                                                                                                                                                                                                                                                                                                                                                                           Sequence 477, Applic Publication No. US20 GENERAL INFORMATION:
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LENGTH: 18
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Best Local Similarity
Matches 15; Conserv
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                                                                        PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/316,630 PRIOR FILING DATE: 1999-05-21 NUMBER OF SEQ ID NOS: 19
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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
                                                                                                                                                                             APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ward, Neil Raymond APPLICANT: Mundy, Christophe
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LENGTH: 408
TYPE: PRT
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Rayner, William Nigel
Naylor, Stuart
                                                                                                                                                                                                                                                                                                            Harris, Robert Alan
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                                                                                                                                                                                                                                                                                              White, Jonathan
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100.0%; F1
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Pred. No.
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ORGANISM: Homo Sapiens

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`き命 protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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102
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143.151 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13 14 15	10 11 12	3 ሬ 4 ይ ወ ር ር	Regult No.
78 76.5 75	87 81 79 79	888888 1777	Score 102
76.5 75.0 73.5	79.4 77.5 77.5	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Query Match
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US-09-836-073-10 US-09-836-073-16 US-09-836-073-2	US-10-836-073-12 US-09-836-073-11 US-09-836-073-11	US-09-836-073-13 US-09-836-073-13 US-09-836-073-14 US-09-836-073-14 US-10-170-385-477 US-09-925-298-695	ID US-09-836-073-4
Sequence 10, Appl Sequence 16, Appl Sequence 2, Appli	4 K	Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 14, Appl Sequence 477, App Sequence 695, App	Description Sequence 4, Appli

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14	14	12	10	9	9	16	12	16	9	14	14	14	10	9	9	14	14	14	12	10	9	9	9	12	9	9	9	15	9
US-10-054-295-26	758-2	-10-325-810-2	-09-438-486-2	66-253-26	-676-2	7-963	424-599	3	US-09-836-073-6	-611-	US-10-054-295-24	-10-053-758-	US-09-438-486-24	US-09-766-253-24	US-09-843-676-24	US-10-054-611-25	-10-054-295-	US-10-053-758-25	US-10-325-810-215	US-09-438-486-25	US-09-766-253-25	US-09-843-676-25	US-09-836-073-19	US-10-325-810-214	9-836-073-8	US-09-836-073-15	US-09-836-073-7	0-3	US-09-836-073-3
sequence 20, Appr	0 0	Sequence 216, App	26	N	26,	e 125		Sequence 184914,	Sequence 6, Appli	24,	Sequence 24, Appl	24,	2	Sequence 24, Appl		Sequence 25, Appl	Sequence 25, Appl	25,	215,	25,	25, 1	Sequence 25, Appl	Sequence 19, Appl	×	œ	5	Sequence 7, Appli	e 20	Sequence 3, Appli

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4
                                                             , Sequence 5, Application US/09836073
; Patent No. US20020173475A1
                                                                                                   RESULT 2
US-09-836-073-5
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GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Marayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
TITLE REFERENCE: 220002054822
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                               1 QQQEAKICHQIEYYFGDF 18
                                                                                                                                                                                    1 QQQEAKICHQIEYYFGDF 18
                                                                                                                                                                                                                                                                      h 100.0%; Score 102; DB 9; Similarity 100.0%; Pred. No. 4.7e-09; 18; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              Length 18;
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APPLICATION NUMBER:

18-APR-1997

US 08/844,419

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CLASSIFICATION: 08/724,643

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECHOMUNICATION INFORMATION:

TELEPHAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acido
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US-09-430-323-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/09430323 Patent No. 6309867 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acida
STRANDEDNESS: not relavoropology: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION UNATA:
APPLICATION UNMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ICHQIEYYFGDF 18
                                                                        APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcadero Center, 8th Floor
                                 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
PPLICATION NUMBER: US 08/844,419
ILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morin, Gregg B.
Harley, Calvin
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Nakamura, Toru
Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.4%; Score 58.5; DB 3; Length 37; 91.7%; Pred. No. 0.008;
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TOPOLOGY: not relevant

HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24
밁
                                                                     Query Match 57.4%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0: INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                  7 ICHQIEYYFGDF 18
ICHQ-EYYFGDF 11
                                                                                                                                                                                                                     LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                  576-0300
                                                                                         Score 58.5; DB 4;
Pred. No. 0.008;
                                                                         Mismatches
                                                                         <u>,</u>
                                                                                                              Length 37;
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Search completed: September 10, 2004, 18:05:08
Job time : 16.8883 secs

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SEQUENCE
US-09-721-456-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-851-843A-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Andrews, William H.
ITLE OF INVENTION: No. 6093809el Telomerase
                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                 FILING DATE: 0
CLASSIFICATION:
                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                    COUNTRY:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                                                                                                                        San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                     California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 38 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELEPHONE: (415) 576-0200
ELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                       E: Townsend and Townsend and Crew LLP Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LING DATE: 14-AUG-1997
                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                        Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cech, Thomas R
                                                                                                                                                                                                                                                                                                                                                                                                                    Chapman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Harley, Calvin
                                                        06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ON NUMBER: US 08/911,312
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                                                                     US/08/851,843A
US 08/846,017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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GENERAL II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/724,643
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LENGTH: 37 amino acids
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APPLICATION NUMBER: US 08/844,419
                                        FILING DATE: 06-MAY-CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                        FILING DATE: 09-MAY-
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2
CLASSIFICATION:
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REGISTRATION NUMBER: 3
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                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
CLASSIFICATION:
             APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                           APPLICATION NUMBER:
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                          Andrews, William H.
/ENTION: No. 6261836el Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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91.7%;
                                                                                           US 08/851,843
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Pred. No. 0.
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US-09-402-181B-215
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Best Local Similarity
Matches 10; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
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TOPOLOGY: not relevant
MOLECULE TYDE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                                               APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 APPLICATION NUMBER: US 08/844,419
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                   APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Ploor
                         APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                FILING DATE:
                                                                                                               FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
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Nakamura, Toru
Chapman, Karen B.
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Pred. No. 0.0069;
0; Mismatches
US 08/854,050
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US-09-721-456-215
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Patent No. 6617110
GENERAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY_AGENT INFORMATION:

ATTORNEY_AGENT INFORMATION:
                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NO. 6617110-2000
CLASSIFICATION: 
    CUNKNOWN>

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
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ADDRESSEE: Townsend and Crew LLP
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                    APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
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  PLICATION NUMBER: US 08/846,017
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Nakamura, Toru
Chapman, Karen B.
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Pred. No. 0.0069;
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RESULT 11

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

14-AUG-1997

US 08/911,312

FILING DATE:

09-MAY-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachi
APPLICANT: Nakamura, Toru
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
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APPLICATION NUMBER: WO PO
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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REGISTRATION NUMBER: 015389-002610US
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                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
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 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER: US 08/915,503
14-AUG-1997
                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                    225
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US 08/851,843
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Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: US-08-854-050-25
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6309867
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.9
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION UDATA:
APPLICATION UDATE: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: 
    CURROWN>
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/08/854,050
    FILING DATE: 09-MAY-1997
    APPLICATION NUMBER: US/08/851,843

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TYPE: amino acid
STRANDEDNESS: not rele
TOPOLOGY: not relevant
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                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                             Andrews, William H. TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
10; Conserv
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                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                            COUNTRY: United States of America
                                                                                                                                                                                                                                               ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                           OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toru
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Pred. No. 0.
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FILING DATE: 14-AUG-1997

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Best Local Similarity
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                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Nakamura, Toru
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                                                                                                                                                                        APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
CLASSIFICATION:
                 APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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SEQUENCE DESCRIPTION: SEQ ID NO: 214:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                     United States of America
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91.7%; Pred. No. 0.
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US-08-974-549A-215
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                                                                COMPUTER: IBM PC COMPACTIBLE
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 05-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 06-MAY-1997
PRIOR DATE: 06-MAY-1997
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
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APPLICANT:
PRIOR APPLICATION NUMBER: US 08/851,843

APPLICATION NUMBER: US 00'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Nakamura, Toru
Chapman, Karen B.
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Pred. No. 0.
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US-09-402-181B-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 214, Application US/09402181B Patent No. 6610839
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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REGISTRATION NUMBER: 36.429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF JUNEAU ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                            APPLICATION NUMBER: US 08/912,951
                                                    APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
                                                                                            FILING DATE: 09-MAY-1997
                                                                                                                 APPLICATION NUMBER: US 08/854,050
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Nakamura, Toru
Chapman, Karen B.
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91.7%;
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Pred. No. 0.00024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-721-456-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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GENERAL INFORMATION:
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PO
FILING DATE: 14-AUG-1997
FILING DATE: 01-CCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415)
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415)
               APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                        APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APPL-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09721456
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Morin, Gregg B.
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Nakamura, Toru
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91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas R
NUMBER: US 08/911,312
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Pred. No. 0.00024;
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> Length 38; Indels

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PRIOR FILING DATE:

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Best Local
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SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                 TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
07/648,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                           FILING DATE: January 31, 1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              FILING DATE: January 31, 1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/472,94
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
                                                                                                                       TELEPHONE: (404)-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                           NAME: Pabst, Patrea L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
           ENGTH: 21 amino acids
YPE: amino acid
TRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/321,427
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2800 One Atlantic Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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inear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.3%; Score 87; DB 3; L
100.0%; Pred. No. 8.7e-08;
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                                                                                                                                                                                                                                                07/472,947
                                                                                                                                        31,284
ER: OMRF114CIP(2)DIV
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Best Local Similarity
Thes 12; Conserve
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; LOCATION:
US-08-475-955-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-974-549A-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
PILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/844,419
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PRIOR APPLICATION DATA:
APPLICATION UNUBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-AUG-
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
Ardrews, William H.
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                                                                                                     UMBER: US 08/915,503
14-AUG-1997
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MBER: WO PCT/US97/17618
01-OCT-1997
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Minimum |
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Perfect score:
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Maximum Match 100%
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2: /cgn2=6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2=6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2=6/ptodata/2/iaa/B_COMB.pep:*
5: /cgn2=6/ptodata/2/iaa/BackfIles1.pep:*
6: /cgn2=6/ptodata/2/iaa/backfIles1.pep:*
       Length
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     GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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                   summaries
Sequence 3, Appli
Sequence 20, Appli
Sequence 214, App
Sequence 214, App
Sequence 214, App
Sequence 215, App
Sequence 25, Appl
Sequence 25, Appl
Sequence 215, Appl
Sequence 215, Appl
Sequence 24, Appl
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Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
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Sequence 216, Appl
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הפחתפוורפ דקיי טאהי	comience 10 April	Patent No. 5245013	Sequence 5, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 13869, A	Sequence 4312, Ap	Sequence 2332, Ap	Sequence 4298, Ap	Sequence 27609, A	Sequence 3, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 24329, A	Sequence 31345, A	12,	Sequence 2, Appli	Sequence 62, Appl

ALIGNMENTS

US-09-316-630-3

Sequence 3, Application Patent No. 6291637

us/09316630

GENERAL INFORMATION:

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SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/32
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/08
PRIOR FILING DATE: 1998-05-22
                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                         Sequence 4, Application US/09316630 Patent No. 6291637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL
TITLE OF INVENTION: SMALL YEAST RNA REVEALS
FILE REFERENCE: 22000-20548.21
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                           Best Local
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               APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL
TITLE OF INVENTION: SMALL YEAST RNA REVEALS
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
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CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: LAF
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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NUMBER: 60/086,527
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                                                                             IRES-MEDIATED TRANSLATION BY CRITICAL RNA-PROTEIN INTERACT
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compound that regulates the activity of one or more of the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity in an animal of one or more of the polymucleotides, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a which is differentially regulated in an animal subjected to pain and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                      kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
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Pred. No.
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SSXSS
Sequence 415 AA;
                                  specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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뭐 S Matches Query Match Best Local Similarity 15; Conservative 14 4 EAKICHQIBYYFGDF 18 EAKICHQIEYYFGDF 28 85.3%; 0 Score 87; pred. No. Mismatches DB 7; 1.1e-05; o ,, Length 415 Indels <u>.</u>

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Search completed: September 10, 2004, 17:51:46
Job time: 57.4128 secs

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RESULT 13
ADE62859
subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypoptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypoptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction in the composition of the polymoptide or the compound that a construction are the compound that a compound the compound are the compound that the compound that are the compound that the compound that are the compound that are the compound that are the compound that the compound that are the compound that the com
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                        injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal
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                                                                                      specification, but was obtained in electronic form directly from WIPO at
                                                    ftp.wipo.int/pub/published_pct_sequences
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
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Query Match 85. Best Local Similarity 100 Matches 15; Conservative

85.3%; 5-100.0%; Pro 0;

Score 87; DB 7; I Pred. No. 1.1e-05; 0; Mismatches 0;

Length 408; Indels

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Sequence 415

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RESULT 14
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                                                                                                                                                                                                                                                                         Cclaimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a cc kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence cc that is differentially expressed in neuronal tissue of a first animal compound that is a method for identifying an agent cc subjected to pain, a method for identifying a compound which regulates cc expression of a polynucleotide sequence which is differentially cc compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the cc polynucleotides, a method for more of the polynucleotides, an enthod for identifying a compound useful in treating cc pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more compound that its activity is useful for preparing a medicament for treating compound activity is useful for preparing a medicament for treating companies its activity is useful for preparing a medicament for treating companies.
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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                  pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the print of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                               specification, but was obtained in electi
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or human polynucleotides or a polynucleotide which represents a fr. derivative or allelic variation of the nucleic acid sequence. Also
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                                                            RESULT 12
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spinal
spared
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                ADE63995 standard; protein; 408 AA
                                                                                                                                                                                                                                                                              Sequence 408
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                                                                                                                                                                                                                      Local
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
                                                                                                                                                          4 EAKICHQIEYYFGDF 18
                                                                                                                                                                                                                    Similarity
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100.0%; Pr
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                                                                                                                                                                                                                    Score 87; DB 7; L; Pred. No. 1.1e-05;
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14

EAKICHQIEYYFGDF

Matches Query Match Best Local

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Conservative

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Similarity

85.3%;

Score 87; DB; Pred. No. 1.1

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Length 408 Indels

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Gaps

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4 EAKICHQIEYYFGDF 18

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Cor human polynucleotides or a polynucleotide which represents a fragment, comprising the work polynucleotide sequence. Also comprising the wector comprising the movel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence comprising the westor, a method for identifying a nucleotide sequence that increases or decreases the expression of the polynucleotide sequence contains a differentially regulated in an animal subjected to pain and a subjected to pain, a method for identifying an agent compound that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of the polynucleotide sequence compound that regulates the activity of one or more of the polynucleotides and the compound or more of the continuity in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a continuity in an animal of one or more of the polypeptides given in the contributes or their antibodies. The polynucleotide given in the conjunction of a pharmaceutical for proparing a medicament for treating pain and a pharmaceutical for proparing a medicament for treating conjunction of the polynucleotide or the compound that regulates the conjunction of the polynucleotide or the compound that regulates the conjunction of the polynucleotide or the compound that regulates the conjunction of the polynucleotide or more of the polynucleotide or the compound that regulates the conjunction of the polynucleotide or the compound that regulates the one or more of the polynucleotide or the conjunction of the polynucleotide or the constriction of the polynucleotide or the polyn
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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Sequence 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENBANK; P05455
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(FARB ) BAYER AG.
                                                                            ftp.wipo.int/pub/published_pct_sequences
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segmental nerve injury; chronic constriction injury; CCI,
nerve injury; SNI; Chung.
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to methods for identifying genes and cc proteins that are implicated in a specific disease or physiological ccondition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a cc second specialised cell type, under two experimental conditions, and cc identifying a gene that is differentially regulated in the two experimental conditions, and comprises under experimental conditions. ABV77873-ABV78116 cc and ABP65061-ABP65257 were identified using the methods of the invention. Cc The coding sequences and proteins are useful for treating a disease in a cc patient, for manufacture of a medicament for treating hypoxia-regulated cc conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful cc condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
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Best Local (
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08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
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                Human;
spinal
spared
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                pain; neuronal tissue; gene therapy; segmental nerve injury; chronic cons nerve injury; SNI; Chung.
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                                                                                                                        (first entry)
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100.0%; Pred. No. 1.1e-05;
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                                    constriction injury; CCI;
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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, clearivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a complex comprising the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotide, a method for producing a pharmaceutical composition, a method for identifying a compound undersome the compound that regulates the cativity in an animal of one or more of the polynucleotide given in the composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more complypeptides or their antibodies. The polynucleotide or the compound that polypeptides or their antibodies. The polynucleotide or the compound that composition comprising a medicament for treating pain (e.g. spinal segmental nerve injury (chung), chronic constriction conjury (chung). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the printed specification will shed not enterprise.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English.
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(FARB )
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Sequence 408
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BAYER AG.
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,Human Protein P05455, SEQ ID NO 11947
                29-JAN-2004
                                                 ADD46272 standard; protein; 408
                                  ADD46272;
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                                                                                           14 EAKICHQIEYYFGDF 28
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                                                                                                                            Similarity
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100.0%; Pred. No.
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Best Local S
Matches 15
                                                                                                                                                                    5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                       Sequence 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
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                               Similarity
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                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0122487P
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                               85.3%; Score 87; DB 3; L
100.0%; Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tag; secreted protein; cDNA isolation;
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Pred. No.
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3.9e-07;
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                                                           Length 92;
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RESULT, 8
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Best Local S
Matches 15
Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                         The human lupus antigen (La) is diagnostic for Sjogren's syndrome, as well as occurring in systemic lupus erthematosus patients. The La protei is clinically related to the Ro protein that is highly common among autoimmune patients. La and Ro antigens sometimes reside on the same cellular ribonucleoprotein particle; most La patients contain some Ro antibodies and vice versa. La cDNA has been isolated from a human liver library. (Updated on 25-MAR-2003 to correct PF field.)
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                                                 Hypoxia-regulated protein
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                                                                                                  ABP65252;
                                                                                                                         ABP65252 standard;
                                                                                                                                                                                                                                                                                   Sequence 408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma overlap syndrome - useful for diagnosis and treatment of autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-362015/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 15-16; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-1996
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12-MAR-1997
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                                                                                                                                                                                                                                               Local Similarity
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(first entry)
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                                                                                                                         protein;
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RESULT 5
ABG72101
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rhabdovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus, coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck and human hepatitis B virus, and vesicular stomatitis virus. The peptide also inhibits replication of the above viruses. The LAP peptide selectively inhibits viral protein translation, and is therefore not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the La autoantigen binding domain (LAP). LAP is a cellular protein which binds to an internal ribosome entry site (IRES). The peptide is used to inhibit mRNA translation, viral protein translation or viral replication. Viral mRNA translation is initiated at the IRES and the LAP peptide prevents translation initiation factors from binding at the site. The peptide can be used alone or in combination with an inhibitor RNA (IRNA see AAZ45200). The LAP peptide is useful as an antiviral agent, which works through the inhibition of mRNA translation, especially viral mRNA. Examples of viruses which can be inhibited are picornavirus, flavivirus, coronavirus, hepatides as of C viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New yeast inhibitory peptide useful for inhibiting viral translation and replication.
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                                                                                                                                                                                 internal ribosome viral life cycle;
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                           16-APR-2001;
                                                                                                               WO200283858-A2
                                                                                                                                         Unidentified.
                                                                                                                                                                    agricultural;
                                                                                                                                                                                                              Viral replication
                                                                                                                                                                                                                                                                      28-JAN-2003
                                                                                                                                                                                                                                                                                                                           ABG72101 standard; peptide; 18
                                                      12-APR-2002; 2002WO-US011589
                                                                                   24-OCT-2002
(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
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                           2001US-00836073
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                       horticultural;
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                                                                                                                                                                                inhibitor; IRBS initiated translation; LAP;
entry site initiated translation; La antigen protein;
antiviral therapy; pharmaceutical; veterinary;
                                                                                                                                                                                                                                         inhibiting
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Pred. No.
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3.9e-07;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blochemical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents
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                                                                                                                                                                                                                                                                                                                                   internal ribosome entry site initiated translation; La antigen protein;
viral life cycle; antiviral therapy; pharmaceutical; veterinary;
agricultural; horticultural; virucide; bovine.
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                                                                                 New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                                                                                                                                                                                                                                         Viral replication
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100.0%; Pr
                                                         19pp;
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Pred. No.
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3.9e-07;
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The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of

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RESULT 2
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             RESULT 3
ABG72113
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                                                                                                                                                                                                                                                                                                                                                          New compound containing acidic and aromatic amino acids, antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
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ABG72113 standard; peptide; 17
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Pred. No. 1.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal ribosome entry site initiated translation; La antigen p viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide; mouse.
                                                                             La autoantigen; LAP; internal ribosome entry site; IRES; translation; viral replication; IRNA; antiviral agent; picornavirus; flavivirus; coronavirus; hepatitis virus; rhabdovirus; adenovirus; coxsackie virus; parainfilenza virus; poliovirus; rhinovirus; encephalomyocarditis virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.
                                                                                                                                                     Human la autoantigen peptide
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                                                                                                                                                                                                              AAY52200;
                                                                                                                                                                                                                                         AAY52200 standard;
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                         Homo sapiens.
                                                     vesicular stomatitis
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                                                                    foot-and-mouth disease virus; echo virus;
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100.0%;
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90.314 Million cell updates/sec
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and is derived Pred. No. is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	ហ	4	ω	N	_	Result No.
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Abg72103 Viral rep						Φ		Aab58987 Breast an	Abg08417 Novel hum	Rat Pi	Rat	Huma	Human	Add46272 Human Pro		Abp65252 Hypoxia-r		Aag01351 Human sec	Abg72114 Viral rep	٠.	_	Abg72113 Viral rep	-		Description

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44	44	44	44	45	46	46	47	48	48	48	52	52	56	57	62	71	72	72	7.5
43.1	43.1	43.1	43.1	44.1	45.1	45.1	46.1	47.1	47.1	47.1	51.0	51.0	54.9	55.9	60.8	69.6	70.6	70.6	/1.6
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ADA55336	ABB89645	ABG27058	ABG72117	ABB59107	ABU43510	ABO23427	ABP70526	AAG47712	AAG47713	AAG47714	ABM72091	ABJ19009	ABG72106	ABB65316	ABG72119	ABG72108	ABG72107	ABG72115	AAK43394
Ada55336	ADD89645	Abg27058	Abg72117	Abb59107	Abu43510	Abo23427	Abp70526	Aag47712	Aag47713	Aag47714	Abm72091	Abj 19009	Abg72106	ADD65316	Abg72119	Abg/2108	Abg/210/	Abg/2115	Tar to to the
Human pro	Human por	•	-	ň	Protein e	Amino aci	Histone a	Arabidops	Arabidops	Arabidops	Staphyloc	Pathogen	viral rep	progopul	Viral rep	•	- ,-	•	ì

ALIGNMENTS

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12-APR-2002; 2002WO-US011589.

16-APR-2001; 2001US-00836073.

(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

Dasgupta A, Das S, Baidya N;

WPI; 2003-058634/05.

New compound containing acidic and aromatic amino acids, useful antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications.

Claim 10; Page 16; 19pp; English.

The present invention relates to peptides and methods of inhibiting the replication of viruses that utilise internal ribosome entry site (IRES) initiated translation, and/or inhibiting viruses that utilise the La antigen protein (LAP) in any phase of their life cycle. The peptides of the invention compete with LAP and inhibit the utilisation of various blockmenical and physiological functions of LAP required for a productive life cycle. The methods and compositions are useful as antiviral therapy in pharmaceutical, veterinary or agricultural/horticultural applications. ABG72101-ABG72119 represent peptides useful as antiviral agents

Sequence 18 AA;

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Search completed: September 10, 2004, 18:11:55 Job time : 41.424 secs

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Sequence 16, Application US/09836073

Patent No. US20020173475A1

GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION. METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822

CURRENT APPLICATION NUMBER: US/09/836,073

CURRENT APPLICATION NUMBER: 009/316,630

PRIOR APPLICATION NUMBER: 09/316,630

PRIOR APPLICATION DATE: 1999-05-21
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US-09-836-073-10
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; ORGANISM: Homo Sapiens
US-09-836-073-12
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US-09-836-073-10
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SEQ ID NO 10
LENGTH: 18
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Patent No. US20020173475A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16
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APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
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                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dasgupta, Asim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Rat
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77.8%;
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Pred. No. 8.3e-06;
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Pred. No. 1.2e-05;
2; Mismatches 2
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GENERAL INFORMATION:

APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Narayan
APPLICANT: Dasdya, Narayan
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION UNMEER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-836-073-2
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US-09-836-073-4
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Best Local :
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Best Local Similarity
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                                                                                               Query Match
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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
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TYPE: PRT
                                                                            Local
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                             4 OAKICHQIQYYFGQF 18
                                                                                Similarity
EAKICHQIEYYFGDF 18
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78.9%;
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72.2%;
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                                                             Score 75; DB 9; 1
Pred. No. 3.7e-05;
2; Mismatches 1;
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Pred. No. 3
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                                                                                               Length 18;
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; ORGANISM: Homo sapiens US-10-102-806-695
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US-10-264-049-2643
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                                                                                                                                    ; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13
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SEQ ID NO 2643
LENGTH: 460
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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                                                                                    Query Match
Best Local Similarity
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CURRENT FILLING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Naraya
                                                                                                                                                                                                                                                                                                                              APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PA133P1
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                                                                                                                                                                                      LENGTH: 17
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nes 15; Conservaring
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 ALEAKICHOIEYYFGDF 17
                                                                                    84.7%;
82.4%;
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83.3%;
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                                                                                     Score 83; DB 9;
Pred. No. 1.8e-06;
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Pred. No. 1.1e-05;
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                                                                     Mismatches
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Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Dasgupta, Asim
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19
SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 11
LENGTH: 18
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                                                                                                                                           Sequence 12, Application U Pacent No. US20020173475A1 GENERAL INFORMATION:
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Patent No. U
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Best Local 9
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APPLICANT: Dasg. S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF THE ORDER OF THE OR
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Best Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
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PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
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14; Conservative
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Pred. No. 3.9e-06;
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Pred. No. 8.3e-06;
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US-09-836-073-14
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 18
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                Publication No.
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TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
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APPLICATION NUMBER: US/10/170,385
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                                 I: Krige, David
INVENTION: ANALYSIS METHOD
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                                                                                  Mundy, Christopher Robe
Kan, On
Harris, Robert Alan
White, Jonathan
Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
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                                                                  Kingsman, Susan Mary
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                                                                                                                                                                                                             Neil Raymond
                                                                                                                                                                                           Christopher Robert
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Pred. No.
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US-09-925-298-695
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US-10-170-385-477
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                                 CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR HILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1900-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 695
LENGTH: 460
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LENGTH: 408
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Best Local :
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Publication No.
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SEQ ID NO 695
LENGTH: 460
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FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
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PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
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Local Similarity 83.3%;
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83.3%; Pred. No. 1.1e-05;
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Pred. No. 9.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-10-102-806-695

4 US-10-264-049-2643
US-09-836-073-13

US-09-836-073-19

US-09-836-073-11

US-09-836-073-12

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                                   Sequence 3, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 477, App
Sequence 695, App
Sequence 2643, App
Sequence 13, Appli
Sequence 11, Appli
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ALIGNMENTS

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RESULT 2
US-09-836-073-1
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL RE
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-836-073-3
Sequence 1, Application US/09836073
Patent NO. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09836073 Patent No. US20020173475A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 98; DB 9; Best Local Similarity 100.0%; Pred. No. 7.2e-09; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                            1 AALQAKICHQIQYYFGQF 18
                                                                                                                                                                                                                                      1 AALQAKICHQIQYYFGQF 18
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

NUMBER: US 08/844,419 18-APR-1997

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US-08-854-050-24
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US-09-430-323-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
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Best Local Similarity
Matches 9; Conserv
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APPLICATION NUMBER: US 01
FILING DATE: 01-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: <UNKnown>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICHQIQYYFGQF 18
    FILING DATE: 25-AFK-133,
APPLICATION NUMBER: US 08/844,419
ETT.ING DATE: 18-APR-1997
On/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICHQ-EYYFGDF 11
                                                                                                  APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                              APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley, Calvin
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75.0%;
NUMBER: US 08/724,643
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Pred. No. 0.2;
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Db
                                                                                                                 TOPOLOGY: not relevant

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24
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                                                              Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                      TELEFAX: (415) 576-0: INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                            7 ICHQIQYYFGQF 18
ICHQ-EYYFGDF 11
                                                                                                                                                                                        LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not rele
                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-OCT-1996
                                                              Conservative
                                                                           50.5%;
75.0%;
                                                                           Score 49.5; DI
Pred. No. 0.2;
                                                                Mismatches
                                                                                             DB 4;
                                                                <u>.</u>
                                                                                             Length 37;
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Search completed: September 10, 2004, 18:05:07 Job time : 15.8883 secs

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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                            STREET: Two Embarcadero Center, CITY: San Francisco
                                                     APPLICATION NUMBER: US/08/851,843A FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                       COUNTRY:
                                       CLASSIFICATION:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 215:
                APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 ICHQIQYYFG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4, Application US/08851843A
6093809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/915,503 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                         California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 38 amino acids
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                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                     Townsend and Townsend and Crew LLP
                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ON NUMBER: US 08/911,312
NTE: 14-AUG-1997
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80.0%;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDENNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph T.
REGISTATION NUMBER: 36,429
REFERENCE DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
           APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/844,419
                                                                                                           FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                          94111
                                                                                                                                                                                                                                                                                                          San Francisco
: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08854050
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
                                                                                                                                                                                                                                                                                                                                             Two Embarcadero Center, 8th
                                                                                                                                                                                                                                                                                           United States of America
                                                                                                                                                                                                                                                                                                                                                                                                          Andrews, William H. JENTION: No. 6261836el Telomerase
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                                                                                                                                                                                                                                                                                                                                                             Townsend and
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                                                                                                                                                                                                                                                                                                                                             Townsend and Crew LLP Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      015389-002930US
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Pred. No. 0
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                                                                                                                                                                                              Version #1.30
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RESULT 11
US-09-402-181B-215
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMBER: 1909/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

OPERIOR APPLICATION DATA:
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                      APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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                    APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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Nakamura, Toru
Chapman, Karen B.
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    Mismatches

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Pred. No. 0.17;
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US-09-721-456-215
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-No. 6617110-2000

CLASSIFICATION NUMBER: US/09/721,650

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WS 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 ICHQIQYYFG 16
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                                                          APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19 NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                    APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: <Unknown>
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Chapman, Karen B.
Morin, Gregg B.
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80.0%;
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Pred. No. 0.17;
US 08/846,017
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PRIOR APPLICATION DATA:

06-MAY-1997

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; MOLECULE TYPE: peptide
US-08-974-549A-215
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Best Local Similarity 80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/912,951
                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: NO. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
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                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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REFERENCE/DOCKET NUMBER: 015389-002610US
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                                                APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Apple, Randolph Ted REGISTRATION NUMBER: 36,4:
                                    CLASSIFICATION:
                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                             San Francisco
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Chapman, Karen B.
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(415) 576-0300
777 TD NO: 215:
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                                                                                                                                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                Townsend and Townsend and Crew LLP o Embarcadero Center, 8th Floor
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 US 08/851,843
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Pred. No. 0.17;
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RESULT 10
US-09-430-323-25
US-09-430-323-25
; Sequence 25, Applicatio
; Sequent No. 6309867
; PATENT INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLCCY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-MAY-1
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                  ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: CURKNOWN>

PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                  Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ICHQIQYYFG 16
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Similarity 80.0%;
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                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, CITY: San Francisco STATE: California
APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                         COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09430323
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Nakamura, Karen B.
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Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                      Floor
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Query Match
Best Local Similarity
Matches 9; Conserve
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Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                  PRIOR APPLICATION DATA:
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
APPLICATION NUMBER: FILING DATE: 18-AF
                                                      CLASSIFICATION:
                                                                           FILING DATE: 25-APR-1997
                                                                                                                                    CLASSIFICATION:
                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 06-MA
                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
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FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TRILEPAY. (415) 576-0200
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SEQUENCE DESCRIPTION: SEQ ID NO: 214:
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STRANDEDNESS: <Unknown>
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APPLICATION NUMBER: WO_PCT/US97/17618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/912,951
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                                                                                                                                                                                                                                                                                                                                 United States of America
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Chapman, Karen B.
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TUMBER: US 08/844,419
18-APR-1997
                                                                                                                                                      06-MAY-1997
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75.0%;
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Pred. No. 0.0059;
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US-08-974-549A-215
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                                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
PILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
APPLICATION NUMBER: US 08/851,843
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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NAME: Apple, Randolph T
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APPLICATION NUMBER: 1
FILING DATE: 01-OCT-
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REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
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                 FILING DATE: 06-MAY-
PRIOR APPLICATION DATA:
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Local Similarity 80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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APPLICATION NUMBER:
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Two Embarcadero Center, Eighth Floor
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Chapman, Karen B.
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                                     06-MAY-1997
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                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
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US 08/854,050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Patent No. 6610839
GENERAL INFORMATION:
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LENGTH: 38 amino acids
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Local Similarity 75.0%;
les 9; Conservative
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CINCTRETENTION OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
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STATE: California
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/844,419 FILING DATE: 18-APR-1997 APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                       APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                         APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                          APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
                APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
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Chapman, Karen B.
Morin, Gregg B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO PCT/US97/17885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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US-09-721-456-214
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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Makamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NO. 6617110-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
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LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                               APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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                      APPLICATION NUMBER: US 08/851,843 FILING DATE: 06-MAY-1997 APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
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75.0%;
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Pred. No. 0.0059;
US 08/911,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-475-955-20
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Best Local
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SOFTWARE: PatentIn V
                                                                                                                              APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabbt, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION: 1070/1073-3704
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APPLICANT: Harley
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PRIOR APPLICATION NUMBER:
                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/648,205 FILING DATE: January 31, 1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         FILING DATE: April 1:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                               SEQUENCE CHARACTERISTICS
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              LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/867, FILING DATE: April 13, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/475,955 FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
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APPLICATION NUMBER: 60/086,527
FILING DATE: 1998-05-22
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6641813
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                                                                                                   (404) -873 -8795
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linear
                                                                                                                     (404) -873 -8794
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                                                                                                                                                                                                                                                                                                                                                                 07/867,819
                                                                                                                                       31,284
ER: OMRF114CIP(2)DIV
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Pred. No. 7
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7.5e-08;
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION UNMER: WO PCT/US97/17
FILING DATE: ^^* WO PCT/US97/17
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 1
FILING DATE: 18-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                        FILING DATE: 25-APR-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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                                                                                 APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                  FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-MAY
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                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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Harley, Calvin B.
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Chapman, Karen B.
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                                                                                                                                                                                                                                                                                                       NUMBER: US 08/846,017
25-APR-1997
                                                                                                                                                                                                                                                                                                                                                         18-APR-1997
                                                                                                                                                                                                     UMBER: US 08/854,050
09-MAY-1997
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06-MAY-1997
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 MBER: WO PCT/US97/17618
01-OCT-1997
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                                                                                                                                                                     US 08/911,312
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    Mismatches

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Pred. No. 0.00049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 21;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                    49.5
49.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                         protein search, using sw model
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      September 10, 2004, 17:43:01; Search time 15.8883 Seconds (without alignments) 58.488 Million cell updates/sec
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     Issued_Patents_AA:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
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US-09-316-630-4
US-08-475-955-20
US-08-974-549A-214
US-09-402-181.B-214
US-09-402-181.B-215
US-08-854-050-25
US-09-430-323-25
US-09-402-181.B-215
US-09-430-323-25
US-09-402-181.B-215
US-09-430-323-24
US-08-854-050-24
US-08-851-843A-24
US-08-854-050-24
US-09-29-36-315
US-09-29-37-5436
US-09-29-37-5436
US-09-29-36-37-8-11
US-08-854-050-26
US-09-28-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-09-38-367-36-6
US-08-854-050-26
US-09-430-323-26
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sequence 3, Appli
sequence 20, Appli
sequence 214, App
sequence 214, App
sequence 214, App
sequence 215, Appl
sequence 215, Appl
sequence 25, Appl
sequence 25, Appl
sequence 215, Appl
sequence 215, Appl
sequence 216, Appl
sequence 24, Appl
sequence 24, Appl
sequence 38, Appl
sequence 38, Appl
sequence 38, Appl
sequence 38, Appl
sequence 31, Appl
sequence 31, Appl
sequence 11, Appl
sequence 61, Appl
sequence 11, Appl
sequence 11, Appl
sequence 11, Appl
sequence 216, Appl
sequence 26, Appl
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US-09-328-352-5851 US-09-883-134-4 US-09-883-134-4 US-09-887-1 US-09-72-833-15 US-09-72-833-15 US-09-72-833-16 US-09-107-532A-6934 US-09-107-532A-6934 US-09-107-532A-6934 US-09-107-532A-6934 US-09-107-532A-6934 US-09-107-532A-6934 US-09-28-7358-25 US-08-793-624-25 US-09-543-681A-6745 US-09-287-354-2 US-09-287-354-3 US-09-287-354-4	4	4	4	4	4	ហ	w	۲	4.	4	4	4	4.	4	4	4	4.	4
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40000000000000000000000000000000000000	, Appli	, Appii	, Appli	5	6/45, AD	25, Appi	25, Appi	25, Appi	229, AD	6934, Ap	16, Appi	•	•	ZJ, ADDI	*	4, Appii		

ALIGNMENTS

RESULT 1 US-09-316-630-3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 199-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SUTTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                      US-09-316-630-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09316630 Patent No. 6291637 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Das, Saumana, APPLICANT: Dasgupta, Asim APPLICANT: Dasgupta, Asim ITITLE OF INVENTION: SMALL YEAST RNA REVEALS TITLE OF INVENTION: SMALL YEAST RNA REVEALS 22000-20548.21
                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                            Sequence 4, Application US/09316630 Patent No. 6291637
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
                                                              APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERPERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548.21
                                                                                                                                                                                                                                                                                                                                                     1 AALQAKICHQIQYYFGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   88.8%;
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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7.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRES-MEDIATED TRANSLATION BY A
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
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Search completed: September 10, 2004, 18:11:54 Job time : 40.424 secs

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APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
FILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 18
TWORD: DDT
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US-09-836-073-10
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US-09-836-073-12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.3%;
Best Local Similarity 83.3%;
                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 Sequence 16, Application US/09836073 Patent No. US20020173475A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                      APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLB OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
PILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILLING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dasgupta, Asim
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Pred. No. 1.5e-05;
1; Mismatches 2
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Pred. No. le-05;
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EAKICHQIEYYFGDF 18

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APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Dasidya, Narayan
ITILE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT ETLING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILLING DATE: 1999-05-21
NUMBER OF SEG ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SECTION 10
SECTION 
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US-09-836-073-4
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                                                                                                                                                                                                           ; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4
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APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09836073
Patent No. US20020173475A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 220002054822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18
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       4 EAQICQUIEYYFGDF 18
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Similarity 72.2%;
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                                                                              Conservative
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84.2%;
                                                                                                       78.1%;
86.7%;
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                                                                                                           Score 75; DB 9;
Pred. No. 4.4e-05;
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Pred. No. 4.4e-05;
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Pred. No. 2.7e-05;
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                                                                                                                                           Length 18
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; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13
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US-10-264-049-2643
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2643
LENGTH: 460
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Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Best Local Similarity
Matches 16; Conserv
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PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09836073 Patent No. US20020173475A1
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                                                                  Matches
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
CURRENT FILING DATE: 2002-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dasgupta, Asim
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ORGANISM: Homo sapiens
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                                                                  15;
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                                 2 ALEAQICQQIEYYFGDF 18
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ALEAKICHQIEYYFGDF 17
                                                                  Conservative
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88.9%;
                                                                              86.5%;
88.2%;
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                                                                                   Score 83; I
Pred. No. 2.
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Pred. No. 1.6e-05;
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                                                                   Mismatches
                                                                                                   DB 9;
                                                                                     .2e-06;
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                                                                                                 Length 17;
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Sequence 9, Application US/09836073

| Patent No. US20020173475A1
| GENERAL INFORMATION:
| APPLICANT: Das | S.
| APPLICANT: Das | S.
| APPLICANT: Das | S.
| APPLICANT: Baidya, Narayan
| TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
| TITLE REFERENCE: 22002054822
| CURRENT APPLICATION NUMBER: US/09/836,073
| CURRENT FILING DATE: 2002-10-24
| PRIOR APPLICATION NUMBER: 09/316,630
| PRIOR FILING DATE: 1999-05-21
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                            RESULT 11
US-09-836-073-12
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US-09-836-073-9
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US-09-836-073-11
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                                                                              Sequence 12, Application Usatent No. US20020173475A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dasgupta, Asim
APPLICANT: Dass, S.
APPLICANT: Baidya, Narayan
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
F.L.S REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
NUMBER OF SEQ ID NOS: 19
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
                      APPLICANT: Dasgupta, Asim APPLICANT: Das, S. APPLICANT: Baidya, Naraya
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TYPE: PRT
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Local Similarity 88.2%;
hes 15; Conservative
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l Similarity 83.3%;
15; Conservative
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                                                                                                                       Application US/09836073
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Pred. No. le-05;
1; Mismatches
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Pred. No. 4.8e-06;
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; ORGANISM: Homo Sapiens
US-09-836-073-1
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                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                              Sequence 477, Application US/10170385 Publication No. US20030203372A1
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
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CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                          APPLICANT:
                                                                                                                                                                                            APPLICANT: Ward, Neil Raymond APPLICANT: Mundy, Christopher
                               APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
                                                                                        APPLICANT:
                                                                                                                       APPLICANT:
                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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APPLICATION NUMBER: US/10/170,385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 90.6%;
1 Similarity 88.9%;
16; Conservative
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                                                                                                                                                                    Mundy, ...
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                                                                                 Binley, Katie Mary
Rayner, William Nigel
Naylor, Stuart
                                                                                                                                    Harris, Robert Alan
White, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09836073
                                                                  Kingsman, Susan Mary
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                          Christopher Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6%;
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Pred. No. 5.36
1; Mismatches
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Pred. No. 5
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT APPLICATION NUMBER: 09/925,298
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 695
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US-09-925-298-695
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US-10-170-385-477
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PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR PLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 477
                                                                                                                                                                                                                                                                                                          Sequence 695, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 695, Applic Publication No. US20 GENERAL INFORMATION:
SEQ ID NO 695
LENGTH: 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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Local Similarity 88.9%;
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11 AALEAKICHQIEYYFGDF 28
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o. US20020039764A1
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Pred. No. 1.6e-05;
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Title:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                          96
87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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4: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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18: /cgm2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
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96
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143.151 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-10-170-385-477
2 US-09-925-298-695
4 US-10-170-806-695
4 US-10-170-806-695
5 US-10-264-049-2643
US-09-836-073-13
US-09-836-073-12
US-09-836-073-16
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US-09-836-073-1
US-09-836-073-14
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                        Sequence 2, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 477, App
Sequence 695, App
Sequence 695, App
Sequence 2643, Appl
Sequence 13, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 3, Appli
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US-10-054-611-26		US-10-053-758-26	-325-810-	US-09-438-486-26	N	843-676-2	-437-963	4	US-10-054-295-24	ι,	8-486-2		US-09-843-676-24	US-10-437-963-128072	US-09-836-073-6	US-09-836-073-19	US-10-325-810-214	-10-054-611-	-10-054-295-	-10-053	0-325-810-	US-09-438-486-25)9-766-253-2	US-09-843-676-25)9-836-073-5	-10-376-121	_	US-09-836-073-7	09-836-073-
Sequence 26, Appl	26,	26,	e 216,	e 26, #	26, 2	•	e 125	2	24,	•	24,	24, 8	N	22	σ	9,	14		25,	25, 7	215,	25, 1		Sequence 25, Appl	5	Œ	, 8	7, A	15,

ALIGNMENTS

RESULT 1 US-09-836-073-2

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APPLICANT: Dasgupta, Asim
APPLICANT: Dasy, S.
APPLICANT: Baidya, Narayan
TITLE Dailya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PAT
ORGANISM: Homo Sapiens
US-09-836-073-2
                                      Sequence 1, Application US/09836073; Patent No. US20020173475A1; GENERAL INFORMATION:
                                                                                                    RESULT 2
US-09:836-073-1
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Patent No. US20020173475A1
                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
APPLICANT: Dasgupta, APPLICANT: Das, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                             1 AALEAQICQQIEYYFGDF 18
                                                                                                                                                                                      1 AALEAQICQQIEYYFGDF 18
                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 9; 1 100.0%; Pred. No. 1.9e-08;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

NUMBER: US 08/844,419 18-APR-1997

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RESULT 15
US-09-430-323-24
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.6
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01531
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US 08/724,643
                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                 APPLICATION NUMBER: US 08/854,050
PILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
PILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
PILING DATE: 18-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09430323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
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US 08/724,643
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TOPOLOGY: not relevant;
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24
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                                                                    Matches
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                         TELEFAX: (415) 576-0: INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                    10;
                         7 ICQQIEYYFGDF 18
ICHO-BYYFGDF 11
                                                                                                                                                                                                       LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
                                                                    Conservative
                                                                                  52.6%; Score 50.5; DB 4; 83.3%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                           576-0300
                                                                    Mismatches
                                                                                                  Length 37;
                                                                    Indels
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                                                                  Gaps
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Search completed: September 10, 2004, 18:05:07 Job time: 17.8883 secs

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; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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                                                                                                                                                                                                                                                                                                          APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERAFE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                      STREET:
                                     CLASSIFICATION
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
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FILING DATE: 14-AUG-1997
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Nakamura, Karen B.
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                                                                                                                                                                                                                              United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas R
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83.3%;
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US 08/846,017
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Pred. No. 0.0029
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es 2; Indels
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Best Local
          FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/724,643
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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CLASSIFICATION:
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CLASSIFICATION:
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Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
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Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                   United States of America
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                                                                                                                                                                                                    Release #1.0, Version #1.30
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Pred. No. 0.
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RESULT 11
US-09-402-181B-214
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 38 amino Type
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Best Local Similarity 83.3%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/HCCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TICCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/TCCT/
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REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                 APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 ICQQIEYYFGDF 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICHOXEYYFGDF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/915,503
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      US 08/854,050
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US-09-721-456-214
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 214, Applicat Patent No. 6617110 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
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SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ICQQIEYYFGDF 18
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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Chapman, Karen B.
Morin, Gregg B.
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Pred. No. 0.0029;
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Matches

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TOPOLOGY: linear;
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MOLECULE TYPE: peptide
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-402-181B-215
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Patent No. 6617110
GENERAL INFORMATION:
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Best Local S
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Chapman, Karen B.
Chapman, Gregg B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
              APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/721,456 FILING DATE: 22-No. 6617110-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                            APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
                                                                                                                                      APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                  FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/724,643
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90.9%;
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Pred. No. 0.002;
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                     015389-002610US
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TOPOLOGY: linear;

MOLECULE TYPE: peptide;
SEQUENCE DESCRIPTION: SUS-09-721-456-215
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Best Local Similarity
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READAL MEDIUM TYPE:
                                                                                                            FILING DATE: 25-APR-1997
PRIOR APPLICATION UNDER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                  PRIOR APPLICATION DATA:
                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 'Iwo ......
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/974,549A FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: FILING DATE: 14-AU
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                APPLICATION NUMBER:
                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I: Andrews, William H.
INVENTION: Human Telomerase Catalytic Subunit
F SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 38 amino acids
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Nakamura, Io.
Nakamura, Karen B.
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Harley, Calvin B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend and Townsend and Crew LLP o Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
IMBER: US 08/912,951
14-AUG-1997
                                                 14-AUG-1997
                                                                                                09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomas R
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                                                                  US 08/911,312
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Pred. No. 0.
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Best Local S
Matches 10
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GENERAL INFORMATION:
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                                                                               INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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STRANDEDNESS: not rele
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 38 amino acids
                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andrews, william H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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STATE: California
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                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
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STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                     LENGTH: 38 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
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Nakamura, Toru
Chapman, Karen B.
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    Mismatches

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Pred. No. 0.002;
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RESULT 8
US-09-402-181B-215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 215, Applicat Patent No. 6610839
GENERAL INFORMATION:
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Best Local Similarity
INFORMATION FOR SEQ ID NO: 215
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-0CT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                      REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/402,181B FILING DATE: 29-Sep-1997 CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                            FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997 APPLICATION NUMBER: US 08/911,312 FILING DATE: 14-AUG-1997
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                                                                                                                                                NAME: Ausenhus, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/912,951
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Harley, Calvin B.
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Nakamura, Toru
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Pred. No. 0.002;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                           FILING DATE: 06-MAY-1997 PRIOR APPLICATION DATA:
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                                              ATTORNEY/AGENT INFORMATION:
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San F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                   APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 18-APF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                        APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997
                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/846,017
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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Andrews, William H.
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18-APR-1997
                         Randolph
                                                                                                                                                      14-AUG-1997
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NUMBER: 015389-002610US
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90`.9%;
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                                                                            WO PCT/US97/17885
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Pred. No. 0.002;
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                           CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                   REFERENCE/DOCKET NUMBER: 01
ELECOMMUNICATION INFORMATION:
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                                                NAME: Apple, Randolph REGISTRATION NUMBER: 36
                                                                                              FILING DATE: 01
CLASSIFICATION:
                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Andrews, William H.
INVENTION: No. 6261836el Telomerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 amino acids
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Harley, Calvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chapman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415)
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N: 536
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                                                                                                                                                                                                                                      25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karen B.
                                                                                                                                                                                                                                                      US 08/846,017
                                                                                                                                                                                                                                                                                                                 US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toru
                                                                                                                              US 08/724,643
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                                              36,429
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    Mismatches

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Pred. No. 0.
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8th Floor
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Best Local S
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SOFTWARE: Patentin V
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APPLICANT: Harley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                  TELEFAX: (404)-873-87:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: B-LAP OTHER INFORMATION: this peptide is biotinylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                               APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
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                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (404)-873-8794
                                                                                                                                                                                                                                    FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                   NAME: Pabst, Patrea L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                 ENGTH:
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                                                                                  (404) -873-8795
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                                                                                                                                               31,284
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Pred. No.
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US-08-851-843A-25
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                                                                                                 INFORMATION FOR SEQ ID NO:
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MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 25-APR-1997
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APPLICANT:
                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPPLICANT: Harley, Calvin
NPPLICANT: Andrews, William H.
NTLE OF INVENTION: No. 6093809el Telomerase
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                                                                                                                                                              NAME: Apple, Randolph 7
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2
CLASSIFICATION:
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nes 11; Conservative
            TOPOLOGY:
                            STRANDEDNESS:
                                             LENGTH: 38 amino acids
TYPE: amino acid
                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: (CLASSIFICATION:
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                                                                                                                                                                                                                                   CLASSIFICATION:
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California
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Chapman, Karen B.
Morin, Gregg B.
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              SS: not relevant not relevant
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8..15
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18-APR-1997
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91.7%;
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                                                                                                                                                                                  36,429
                                                                                                                                                                    015389-002930US
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Pred. No. 0.
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4 US-09-430-323-25

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6 US-09-430-323-26

6 US-09-430-323-26

8 US-09-421-456-216

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9 US-08-451-778A-33

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9 US-09-4314-000C-3435

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Sequence 3, Appli
Sequence 20, Appli
Sequence 25, Appl
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Sequence 25, Appl
Sequence 25, Appl
Sequence 215, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 26, Appl
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Sequence 27, Appl
Sequence 21, Appl
Sequence 31, Appl
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
ITILE OF INVENTION: INTERFERENCE WITH VIRAL IR
ITILE OF INVENTION: SMALL YEAST RNA REVEALS CR
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
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CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR FILING DATE: 1997-10-06
PRIOR FILING DATE: 1994-10-16
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.1
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SEQ ID NO 3
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                                                                                                                                                                                                          Sequence 4, Application US/09316630
Patent No. 6291637
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APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL
TITLE OF INVENTION: SMALL YEAST RNA REVEALS
FILE REFERENCE: 22000-20548.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 4.1e-08;
1; Mismatches 1
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McGarry, Sean

To: Subject: STIC-Biotech/ChemLib SEQ SEARCH 09/836,073

Sean McGarry 73484 AU 1635 REM 02D19 Office REM 2C18 Mailbox X20761

Please search a. a. SEQ ID NOS: 2-4, 12, and 14-19.

Thank You